

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 21, 2004, 09:59:59 ; Search time 13 Seconds  
(without alignments)  
640.863 Million cell updates/sec

Title: US-10-031-607-7  
Perfect score: 913  
Sequence: 1 WRLPLQCVLWGLLTAVHP.....WLCNRQATRLMLSVPRIG 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	795	86.0	277	1	TNR5_HUMAN
2	588	61.1	269	1	TNR5_BOVIN
3	483	52.9	289	1	TNR5_MOUSE
4	262	28.7	625	1	TR11_MOUSE
5	259	28.4	616	1	TR11_HUMAN
6	212.5	23.3	461	1	TR1B_HUMAN
7	202	22.1	283	1	TR1A_HUMAN
8	200	21.9	435	1	TNR3_HUMAN
9	188.5	20.6	324	1	TNR6_RAT
10	181	19.8	401	1	T11B_RAT
11	180	19.7	327	1	TNR6_MOUSE
12	177	19.4	401	1	T11B_HUMAN
13	175	19.2	401	1	T11B_MOUSE
14	173	18.9	474	1	TR1B_MOUSE
15	170	18.6	349	1	CRMB_VARY
16	169	18.5	323	1	TNR6_BOVIN
17	168	18.4	349	1	CRMB_CAMPS
18	165	18.1	332	1	TNR6_PIG
19	165	18.1	335	1	TNR6_HUMAN
20	164	18.0	204	1	TR26_MOUSE
21	163	17.9	351	1	CRMB_COMX
22	162.5	17.8	280	1	TNR7_HUMAN
23	153	16.8	415	1	TNR3_MOUSE
24	151	16.5	250	1	TNR7_MOUSE
25	145	15.9	271	1	TNR4_RAT
26	142	15.6	272	1	TNR4_MOUSE
27	135.5	14.8	277	1	TNR4_HUMAN
28	130	14.2	416	1	TR16_CHICK
29	129.5	14.2	461	1	TR1A_RAT
30	129	14.1	326	1	VT2_MYXVL
31	128.5	14.1	454	1	TR1A_MOUSE
32	125.5	13.7	455	1	TR1A_HUMAN
33	125	13.7	417	1	TR25_HUMAN

34	124	13.6	830	1	SREC_HUMAN	Q14162 homo sapien
35	122	13.4	300	1	TR6B_HUMAN	Q95407 homo sapien
36	116	12.7	325	1	VT2_SFVKA	P25943 shope fibro
37	115.5	12.7	427	1	TR16_HUMAN	P08138 homo sapien
38	114.5	12.5	417	1	TR16_MOUSE	Q920w1 mus musculus
39	110	12.0	514	1	EDAR_ORYLA	Q90VY2 oryzias lat
40	109.5	12.0	461	1	TR1A_PIG	P50855 sus scrofa
41	108.5	11.9	425	1	TR16_RAT	P07174 rattus norv
42	107	11.7	833	1	DL_DROME	P10041 drosophila
43	107	11.7	1790	1	LMBI_DROME	F11046 drosophila
44	106	11.6	1587	1	LMG3_HUMAN	Q9Y6N6 homo sapien
45	105	11.5	471	1	TR1A_BOVIN	O19131 bos taurus

ALIGNMENTS

RESULT 1					
TNR5_HUMAN					
ID	TNR5_HUMAN	STANDARD;	PRT;	277	AA.
AC	P25942; Q9BYU0;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	01-MAY-1992 (Rel. 22, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).				
GN	TNFRSF5 OR CD40.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
[1]					
RP	SEQUENCE FROM N.A. (ISOFORM I).				
RA	MEDLINE=89356608; PubMed=2475341;				
RA	Stamenkovic I., Clark E.A., Seed B.;				
RT	"A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";				
RL	EMBO J. 8:1403-1410(1989).				
[2]					
RP	SEQUENCE FROM N.A. (ISOFORM I).				
RA	MEDLINE=21638749; PubMed=11780052;				
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,				
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,				
RA	Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,				
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,				
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,				
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,				
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby M.R.,				
RA	Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,				
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,				
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,				
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,				
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,				
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,				
RA	Lehvaeslahti M.H., Levensha M.A., Lloyd J., Lloyd D.M., Lovell J.D.,				
RA	Marsh V.L., Martin S.L., McConachie I.J., McClay K., McMurray A.A.,				
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,				
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,				
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,				
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,				
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,				
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,				
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,				
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,				
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,				
RT	"The DNA sequence and comparative analysis of human chromosome 20.";				
RL	Nature 414:865-871(2001).				
[3]					
RP	SEQUENCE FROM N.A. (ISOFORM II).				
RA	MEDLINE=21117110; PubMed=11172023;				
RA	Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;				
RT	"Regulation of CD40 function by its isoforms generated through				

RT alternative splicing.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM I).  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.A., Lequellano N.A., McKernan K.J., Abranson R.D., Mullany S.J.,  
RA Bosak S.A., McQuinn F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Wuzley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP INTERACTION WITH TRAF3.  
RX MEDLINE=95184010; PubMed=7533327;  
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;  
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";  
RL Science 267:1494-1498(1995).  
RN [6]  
RP INTERACTION WITH TRAF3.  
RX MEDLINE=9512692; PubMed=7530216;  
RA Sato T., Irie S., Reed J.C.;  
RT "A novel member of the TRAF family of putative signal transducing  
RT proteins binds to the cytosolic domain of CD40.";  
RL FEBS Lett. 358:113-118(1995).  
RN [7]  
RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.  
RX MEDLINE=98384149; PubMed=9718306;  
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,  
RA Kenry M.R.;  
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)  
RT interactions: regulation of CD40 signaling through multiple TRAF  
RT binding sites and TRAF hetero-oligomerization.";  
RL Biochemistry 37:11836-11845(1998).  
RN [8]  
RP INTERACTION WITH TRAF5.  
RX MEDLINE=98172745; PubMed=9511754;  
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Hirai M.,  
RA Otsuka M., Yamamoto T., Inoue J.-I.;  
RT "Cloning and characterization of a cDNA encoding the human homolog of  
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
RL Gene 207:135-140(1998).  
RN [9]  
RP INTERACTION WITH TRAF6.  
RX MEDLINE=98095703; PubMed=9432981;  
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,  
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;  
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates  
RT extracellular signal-regulated kinase (ERK) activity in CD40  
RT signaling along a ras-independent pathway.";  
RL J. Exp. Med. 187:237-244(1998).  
RN [10]  
RP 3D-STRUCTURE MODELING OF 24-144.  
RX MEDLINE=97189482; PubMed=9037712;  
RA Bajorath J., Aruffo A.;  
RT "Construction and analysis of a detailed three-dimensional model of  
RT the ligand binding domain of the human B cell receptor CD40.";  
RL Proteins 27:59-70(1997).  
RN [11]

RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
RX MEDLINE=98266353; PubMed=9605317;  
RA Singh J., Garber B., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
RA Zheng Z., Naismith J.H., Thomas D.;  
RT "The role of polar interactions in the molecular recognition of CD40L  
RT with its receptor CD40.";  
RL Protein Sci. 7:1124-1135(1998).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH  
RP TRAF3.  
RX MEDLINE=20442386; PubMed=10984535;  
RA Ni C.Z., Welsh K., Leo E., Chlou C.K., Wu H., Reed J.C., Ely K.R.;  
RT "Molecular basis for CD40 signaling mediated by TRAF3.";  
RN Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH  
RP TRAF3.  
RX MEDLINE=22000222; PubMed=12005438;  
RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,  
RA Satterthwait A.C., Cheng G., Ely K.R.;  
RT "Downstream regulator TRAF3 binds to the CD40 recognition site on  
RT TRAF3.";  
RL Structure 10:403-411(2002).  
RN [14]  
RP VARIANT HIGH3 ARG-83.  
RX MEDLINE=21532985; PubMed=11675497;  
RA Ferrari S., Gilliani S., Insalaco A., Al-Chonaim A., Soresina A.R.,  
RA Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,  
RA Levy Y., Catalani N., Durandy A., Tbakhi A., Notarangelo L.D.,  
RA Plebani A.;  
RT "Mutations of CD40 gene cause an autosomal recessive form of  
RT immunodeficiency with hyper IgM.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).  
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.  
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);  
CC secreted (isoform II).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Comment=Additional isoforms seem to exist;  
CC Name=I;  
CC IsoId=P25942-1; Sequence=Displayed;  
CC Name=II;  
CC IsoId=P25942-2; Sequence=VSP\_006472, VSP\_006473;  
CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.  
CC -!- DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM  
CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an  
CC autosomal recessive disorder which includes an inability of B  
CC cells to undergo isotype switching, one of the final  
CC differentiation steps in the humoral immune system, and a lack of  
CC germinal center formation.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- DATABASE: NAME=PROT; NOTE=CD guide CD40 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".  
CC  
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CC  
CC EMBL; X60592; CAA43045.1; -;  
CC EMBL; AL035662; CAC17670.1; -;  
CC EMBL; AJ300189; CAC29424.1; -;  
CC EMBL; BC012419; AAH12419.1; -;  
CC PIR; S04460; A60771.  
CC PDB; 1CDF; 01-APR-97.  
CC PDB; 1FLL; 18-OCT-00.  
CC PDB; 1LOA; 08-FEB-00.  
CC PDB; 1CZZ; 26-SEP-01.

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Query Match      86.0%; Score 785; DB 1; Length 277;
Best Local Similarity 95.1%; Pred. No. 5.7e-65;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPPEPTACREKQYLINSQCCLQCPGQKLVSDCTFTETEC 60
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1 MVRPLQCVLWGCLLTAVHPPEPTACREKQYLINSQCCLQCPGQKLVSDCTFTETEC 60
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:

QY 61 PGSESEFLDTWNRETHCHQHKYCDNPLGLRVQOKGTSETDICTCEGWHCTSEACSCV 120
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 PGSESEFLDTWNRETHCHQHKYCDNPLGLRVQOKGTSETDICTCEGWHCTSEACSCV 120
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QY 121 LHRSCSPGFGVKQIAVRPKTLC 143
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 121 LHRSCSPGFGVKQIATGVSDTIC 143
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:

RESULT 2
TNR5_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN TNFRSF5 OR CD40.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97281252; PubMed=9135560;
RA Hirano A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle.";
RL Immunology 90:294-300(1997).
CC -!- FUNCTION: Receptor for TNFRSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity). LOCATION: Type I membrane protein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57745; AAC48710.1; --
DR KSSP; P25942; 1CDF.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >269 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 5.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
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FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT DISULFID 26 37 BY SIMILARITY.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 269
SQ SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match      61.1%; Score 558; DB 1; Length 269;
Best Local Similarity 69.6%; Pred. No. 3.4e-44;
Matches 94; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPPEPTACREKQYLINSQCCLQCPGQKLVSDCTFTETEC 60
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 1 MVRPLQCVLWGCLLTAVHPPEPTACREKQYLINSQCCLQCPGQKLVSDCTFTETEC 60
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:

QY 61 PGSESEFLDTWNRETHCHQHKYCDNPLGLRVQOKGTSETDICTCEGWHCTSEACSCV 120
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 SCGGEFLSTWNRKCYCHEHRYCNPNLGLRIQSEGLTNTDTICVCEGQHCTSHTCESCT 120
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:

QY 121 LHRSCSPGFGVKQIA 135
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 121 PHSCLPFGVGKQIA 135
    |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:

RESULT 3
TNR5_MOUSE STANDARD; PRT; 289 AA.
AC P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92105763; PubMed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
RT species of murine CD40 upon B lymphocyte activation.";
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RP STRAIN=BALB/c;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX STRAIN=BALB/c; TISSUE=Liver;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL J. Immunol. 149:3921-3926(1992).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND
RP V).
RX MEDLINE=21117110; PubMed=11172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.";
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RN Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
[5]
RN INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=753327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
[6]
RN INTERACTION WITH TRAF5.
RX MEDLINE=96382484; PubMed=8790348;
RA Ishida T., Tejo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,
RA Yamamoto T., Inoue J.-I.;
RT TRAF5, a novel tumor necrosis factor receptor-associated factor
RT family protein, mediates CD40 signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
CC -!- FUNCTION: Receptor for TNFSF5/CD40L.
CC -!- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,
CC TRAF2 and TRAF6 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV
CC and V); secreted (isoform II).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=I;
CC IsoId=p27512-1; Sequence=Displayed;
CC Name=II;
CC IsoId=p27512-2; Sequence=VSP_006474, VSP_006475;
CC Name=III;
CC IsoId=p27512-3; Sequence=VSP_006477, VSP_006478;
CC Name=IV;
CC IsoId=p27512-4; Sequence=VSP_006479, VSP_006480;
CC Name=V;
CC IsoId=p27512-5; Sequence=VSP_006476;
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83312; AAB08705.1; -.
DR EMBL; M94126; AAA37404.1; -.
DR EMBL; M94129; AAA37404.1; JOINED.
DR EMBL; M94128; AAA37404.1; JOINED.
DR EMBL; M94127; AAA37404.1; JOINED.
DR EMBL; AJ401387; CAC29427.1; -.
DR EMBL; AJ401388; CAC29428.1; -.
DR EMBL; AJ401389; CAC29429.1; -.
DR EMBL; AJ401390; CAC29430.1; -.
DR PIR; A46476; A46476.
DR HSP; P25942; 1CDF.
DR MGD; MGI188336; Tnfirs5.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1
FT CHAIN 20 289
FT -----
FT DOMAIN 20 193
FT SUPERFAMILY MEMBER 5.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215
FT DONAIN 216 289
FT REPEAT 25 60
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187

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FT DISULFID 26 37 BY SIMILARITY.
FT DISULFID 38 51 BY SIMILARITY.
FT DISULFID 41 59 BY SIMILARITY.
FT DISULFID 62 77 BY SIMILARITY.
FT DISULFID 83 103 BY SIMILARITY.
FT DISULFID 105 119 BY SIMILARITY.
FT DISULFID 111 116 BY SIMILARITY.
FT DISULFID 125 143 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARSPLIC 166 203 SCEDKLEVLQKQTSQTVICGLKSRMALLIVPWVG ->
FT (in isoform II).
FT (FTId=VSP_006474.
FT Missing (in isoform II).
FT VARSPLIC 204 289 /FTId=VSP_006475.
FT VARSPLIC 187 216 GLKSSMRALLIVPVVMGILIIIFGVFLVIK -> E (in
FT isoform V)
FT (FTId=VSP_006476.
FT VARSPLIC 216 234 KKVVKPKDNEMLPAAAR -> SECSEEREEGGFSPEPA
FT S (in isoform III).
FT (FTId=VSP_006477.
FT VARSPLIC 235 289 Missing (in isoform III).
FT VARSPLIC 216 222 /FTId=VSP_006478.
FT VARSPLIC 223 289 KKVVKKP -> SGOETKG (in isoform IV).
FT (FTId=VSP_006479.
FT Missing (in isoform IV).
FT (FTId=VSP_006480.
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;
Query Match 52.9%; Score 483; DB 1; Length 289;
Best Local Similarity 54.9%; Pred. No. 2.6e-37;
Matches 79; Conservative 21; Mismatches 44; Indels 0; Gaps 0;
QY 1 MVRLEQCVLGMCLLTAVHPPEPTACREKQYLINSQCSCLOPQKLVSDCTETETECL 60
Db 1 MVSRLCALMGCLLTAVHLGQCVTCSDKQVLDGQCDLQPGSRLTSHCTALEKTQCH 60
QY 61 PGGESEFLDTWNRETHCHQHKYCDPNLGRVQOQGTSETDTICTCEGHWCTACRSCV 120
Db 61 PCDSGEFSAQWNRREIRCHQHRHCEPNOGLRVKSGTAESDTVCTCKGQHCTSKDCRACA 120
QY 121 LHRSCSPGFGVKQIAVRPKTWLCN 144
Db 121 QHTPCIPGFGVWENATETDTIVCH 144
RESULT 4
TRIL MOUSE
ID TR11 MOUSE STANDARD; PRT; 625 AA.
AC O35305; Q8VCT7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Petal liver;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RN SEQUENCE FROM N.A.

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RC TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodargren B.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
RN [3].  
RP FUNCTION.  
RX MEDLINE=99097247; PubMed=9878548;  
RA Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
RA Morinaga T., Higashio K.;  
RT "RANK is the essential signaling receptor for osteoclast  
differentiation factor in osteoclastogenesis";  
RL Biochem. Biophys. Res. Commun. 253:393-400(1998).  
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRAF6/OPGL; essential for  
RANKL-mediated osteoclastogenesis. Involved in the regulation of  
interactions between T-cells and dendritic cells.  
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By  
similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in  
TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.  
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR ENBL; AF019046; AB86810.1; -;  
DR ENBL; BC019185; AAH19185.1; -;  
DR HSSP; P25942; ICDF.  
DR MGD; MG1:1314891; Tnfrsf11a.  
DR GO; GO:0007275; P:development; IMP.  
DR GO; GO:0007515; P:lymph gland development; IMP.  
DR GO; GO:0001503; P:ossification; IMP.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 625 TUMOR NECROSIS FACTOR RECEPTOR  
SUPERFAMILY MEMBER 11A.  
FT FT 31 214 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 215 234 POTENTIAL.  
FT TRANSMEM 235 625 CYTOPLASMIC (POTENTIAL).  
FT FT 35 69 TNFR-CYS 1.  
FT REPEAT 72 113 TNFR-CYS 2.  
FT REPEAT 115 152 TNFR-CYS 3.  
FT REPEAT 155 195 TNFR-CYS 4.  
FT FT 35 47 BY SIMILARITY.

FT DISULFID 48 61 BY SIMILARITY.  
FT DISULFID 51 69 BY SIMILARITY.  
FT DISULFID 72 87 BY SIMILARITY.  
FT DISULFID 93 113 BY SIMILARITY.  
FT DISULFID 115 128 BY SIMILARITY.  
FT DISULFID 134 152 BY SIMILARITY.  
FT DISULFID 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 494 494 R -> K (IN REF. 2).  
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511DBE CRC64;  
  
Query Match 28.7%; Score 262; DB 1; Length 625;  
Best Local Similarity 38.2%; Pred. No. 9.6e-17;  
Matches 52; Conservative 16; Mismatches 66; Indels 2; Gaps 2;  
  
QY 8 CVLWGCLLTAVHPEPTACREKQVLYNSQCCLSCOPQKLVSDCTETETELCPGSEF 67  
Db 19 CVLVLPVQVTLQVTPP-CTQERHYEHLGRCSRCEPKYLSKCTPTSDVCLPCGDEY 77  
QY 68 LDTWNRETHCHQHKYCDPNTGLRVQOKGTSETDTICTCEEGWHCTSPACSVLHRCSP 127  
Db 78 LDTWNEEDKCLLHKVCDAGKALVAVDPGNHTAPRRCACTAGYHNSD-CCECRRENTCAP 136  
QY 128 GFGYKQTAVRPKTWLC 143  
Db 137 GFGAQHPLQLNKOTVC 152  
  
RESULT 5  
TR11 HUMAN  
ID TR11\_HUMAN STANDARD; PRT; 616 AA.  
AC Q9V6Q6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 11A precursor  
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor  
receptor) (CDPR).  
GN TNFRSF11A OR RANK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Dendritic cell;  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
and dendritic-cell function";  
RL Nature 390:175-179(1997).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=99097247; PubMed=9878548;  
RA Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
RA Morinaga T., Higashio K.;  
RT "RANK is the essential signaling receptor for osteoclast  
differentiation factor in osteoclastogenesis";  
RL Biochem. Biophys. Res. Commun. 253:393-400(1998).  
RN [3]  
RP INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.  
RX MEDLINE=98447691; PubMed=9774460;  
RA Wong B.R., Josien R., Lee S.Y., Vologodskaya M., Steinman R.M.,  
RA Choi Y.;  
RT "The TRAF family of signal transducers mediates NF-kappaB activation  
by the TRANCE receptor";  
RN J. Biol. Chem. 273:28355-28359(1998).  
RN [4]  
RP VARIANT FE0 LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2  
ALA-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.  
RX MEDLINE=20082806; PubMed=10615125;

RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,  
 RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,  
 RA Anderson D.M.;  
 RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause  
 RT familial expansile osteolysis.";  
 RL Nat. Genet. 24:45-48(2000).  
 CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANSC/OPGL; essential for  
 CC RANKL-mediated osteoclastogenesis. Involved in the regulation of  
 CC interactions between T-cells and dendritic cells.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in  
 CC skeletal muscle, thymus, liver, colon, small intestine and adrenal  
 CC gland.  
 CC -!- DISEASE: Defects in TNFRSF11A are the cause of familial expansile  
 CC osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant  
 CC bone disorder characterized by focal areas of increased bone  
 CC remodelling. The osteolytic lesions develop usually in the long  
 CC bones during early adulthood. FEO is often associated with early  
 CC onset deafness and loss of dentition.  
 CC -!- DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone  
 CC 2 (PDB2) [MIM:602080]; also known as familial Paget disease of  
 CC bone. PDB2 is a bone remodelling disorder with clinical  
 CC similarities to FEO. Unlike FEO, however, affected individuals  
 CC have involvement of the axial skeleton with lesions in the spine,  
 CC pelvis and skull.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC  
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 CC  
 DR EMBL; AF018253; AAB86809.1; -.  
 DR HSSP; P25942; 1CDF.  
 DR Genew; HGNC:11908; TNFRSF11A.  
 DR MIM; 603499; -.  
 DR MIM; 174810; -.  
 DR MIM; 602080; -.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
 KW Disease mutation; Deafness.  
 FT SIGNAL 1 29 POTENTIAL.  
 FT CHAIN 30 616 TUMOR NECROSIS FACTOR RECEPTOR  
 FT SUPERFAMILY MEMBER 11A.  
 FT DOMAIN 30 212 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 213 233 POTENTIAL.  
 FT DOMAIN 234 616 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 34 68 TNFR-CYS 1.  
 FT REPEAT 71 112 TNFR-CYS 2.  
 FT REPEAT 114 151 TNFR-CYS 3.  
 FT REPEAT 154 194 TNFR-CYS 4.  
 FT REPEAT 34 46 BY SIMILARITY.  
 FT DISULFID 47 60 BY SIMILARITY.  
 FT DISULFID 50 68 BY SIMILARITY.  
 FT DISULFID 71 86 BY SIMILARITY.  
 FT DISULFID 92 112 BY SIMILARITY.  
 FT DISULFID 114 127 BY SIMILARITY.  
 FT DISULFID 133 151 BY SIMILARITY.  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT VARIANT 21 21 L -> LALLLCALL (in PDB2).

FT VARIANT 21 21 /FTID=VAR\_011516.  
 FT L -> LLLCALL (in FEO).  
 FT /FTID=VAR\_011517.  
 FT VARIANT 192 192 A -> V.  
 FT /FTID=VAR\_011518.  
 SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;  
 Query Match 28.4%; Score 259; DB 1; Length 616;  
 Best Local Similarity 37.9%; Pred. No. 1.8e-16;  
 Matches 53; Conservative 17; Mismatches 68; Indels 2; Gaps 2;  
 QY 4 LPLOQVLMGCLLTAVHPPEPTACREKQYLINSQCCLCPQKLVSDCTETETECPLCG 63  
 Db 14 LLLLCALLARLQVALQIAPP-CTSEKHYEHLGRCCNKCEPGKYMSSKCTTTSDSVCLPCG 72  
 QY 64 ESEFDTWNRETHCHQHKYCDPNLGLRVQKGTSETDITCTCEGWHCTSEACSCVLHR 123  
 Db 73 PDEYLDNNEEDKCLLHKVCDTGKALVAVAGNSTTPRCACCTAGYH-WSQDCECCRRNT 131  
 QY 124 SCSPGFGVKQIARPRXTWLC 143  
 Db 132 ECAPGLGAQHPLQLNKDTVC 151  
 RESULT 6  
 TRIB\_HUMAN STANDARD; PRT; 461 AA.  
 ID TR1B\_HUMAN  
 AC P20333; Q16042; Q9UHI1;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor  
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Stanercept)  
 DE [Contents: Tumor necrosis factor binding protein 2 (TEPII)].  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT ARG-196.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; PubMed=8661109;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND  
 RP ARG-301.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PNS;

RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.A., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RL human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [16]  
RX SEQUENCE OF 37-461 FROM N.A.  
RP MEDLINE=91370690; PubMed=1966549;  
RX Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
RA Brocchius M., Lesslauer W.;  
RT "Two human TNF receptors have similar extracellular, but distinct  
RT intracellular, domain sequences.";  
RL Cytokine 2:231-237 (1990).  
RN [17]  
RX SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.  
RX MEDLINE=90349572; PubMed=2166946;  
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
RA Ringold G.M.;  
RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
RT and demonstration of a shed form of the receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155 (1990).  
RN [18]  
RX SEQUENCE OF 154-193 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21069356; PubMed=11197692;  
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
RT "New single nucleotide polymorphisms in the coding region of human  
RT TNFR2: association with systemic lupus erythematosus.";  
RL Genes Immun. 1:501-503 (2000).  
RN [19]  
RX SEQUENCE OF 27-31.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536 (1990).  
RN [10]  
RX SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
RX MEDLINE=91056048; PubMed=2173696;  
RA Loetscher H., Schlaefer E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
RA Brocchius M.;  
RT "Purification and partial amino acid sequence analysis of two  
RT distinct tumor necrosis factor receptors from HL60 cells.";  
RL J. Biol. Chem. 265:20131-20138 (1990).  
RN [11]  
RX CHARACTERIZATION.  
RX MEDLINE=93016040; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
RA Lipari M.T., Goeddel D.V.;  
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
RT Characterization of ligand binding, internalization, and receptor  
RT phosphorylation.";  
RL J. Biol. Chem. 267:21172-21178 (1992).  
RN [12]  
RX INTERACTION WITH TRAF2.  
RX MEDLINE=94349371; PubMed=8065916;  
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;  
RT "A novel family of putative signal transducers associated with the  
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";  
RL Cell 78:681-692 (1994).  
RN [13]  
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
RP TRAF2.  
RX MEDLINE=99221490; PubMed=10206649;  
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
RT "Structural basis for self-association and receptor recognition of  
RT human TRAF2.";  
RL Nature 398:533-538 (1999).  
RN [14]  
RX VARIANTS ARG-196 AND LYS-232.  
RX MEDLINE=21603988; PubMed=11762942;  
RA Morita C., Horiuchi T., Tsukamoto H., Hatta N., Kikuchi Y.,  
RA Arinobu Y., Otsuka T., Sawabe T., Haraahina S., Nagasawa K., Niho Y.;  
RT "Association of tumor necrosis factor receptor type II polymorphism  
RT 196R with systemic lupus erythematosus in the Japanese: molecular and  
RT functional analysis.";  
RL Arthritis Rheum. 44:2819-2827 (2001).  
RN [15]  
RX VARIANT ARG-196.  
RX MEDLINE=22151311; PubMed=12161545;  
RA Peral B., San Millan J.L., Castello R., Moghetti P.,  
RA Escobar-Morreale H.F.;  
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the  
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic  
RT ovary syndrome and hyperandrogenism.";  
RL J. Clin. Endocrinol. Metab. 87:3977-3983 (2002).  
CC -!- FUNCTION: Receptor with high affinity for homotrimeric  
CC approximately 5-fold lower affinity for homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The TRAF1/2 complex recruits the  
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF  
CC receptor 2 mediates most of the metabolic effects of TNF-alpha.  
CC -!- SUBUNIT: Binds to TRAF2.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- PTM: Phosphorylated; mainly on serine residues and with a very low  
CC level on threonine residues.  
CC -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is  
CC produced from the membrane form by proteolytic processing.  
CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and  
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding  
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to  
CC TNF-alpha and blocks its interactions with receptors.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm"  
CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
CC WWW="http://www.enbrel.com/"

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EMBL; M32315; AAC59929.1; -  
EMBL; U52165; AAC50622.1; -  
EMBL; U52156; AAC50622.1; JOINED.  
EMBL; U52157; AAC50622.1; JOINED.  
EMBL; U52158; AAC50622.1; JOINED.  
EMBL; U52159; AAC50622.1; JOINED.  
EMBL; U52160; AAC50622.1; JOINED.  
EMBL; U52161; AAC50622.1; JOINED.  
EMBL; U52162; AAC50622.1; JOINED.  
EMBL; U52163; AAC50622.1; JOINED.  
EMBL; U52164; AAC50622.1; JOINED.  
EMBL; M55994; AAA36755.1; -  
EMBL; AY264804; AAC89076.1; -  
EMBL; AY342040; AAP88939.1; -

DR EMBL; BC052977; AAH52977.1; --  
 DR EMBL; S63368; AAL19824.2; --  
 DR EMBL; M35857; AAA63262.1; --  
 DR EMBL; AB030950; BAA89053.1; --  
 DR PIR; A35356; A35356.  
 DR PDB; 1CA9; 12-APR-99.  
 DR Genew; HGNC:11917; TNFRSF1B.

Query Match 23.3%; Score 212.5; DB 1; Length 461;  
 Best Local Similarity 34.5%; Pred. No. 2.4e-12;  
 Matches 51; Conservative 12; Mismatches 58; Indels 27; Gaps 6;

QY 4 LPQCVMGLLTAVHPPTACEKQVLYNS--CCSLCQPGKGLVSDCTEFTEICLP 61  
 DB 23 LPAQVA-----FTYAPPGSTCLREYDQTAQMCCKSPGQAKVFTKTSIDTVCD 77  
 QY 62 CGSEFELDTWRETHCHQHKYCDNGLRVQ-----QKGTSEFDTTCTCEGWHCT--- 112  
 DB 78 CEDSTYTLQNMWVPEC-----LSCGRCSDDQVETQACTREONRICTCRPGWICALSK 130  
 QY 113 SEACESCVLHSCSPFGVGVQIAVRPKT 140  
 DB 131 QEGRLCAPLKKCPRGV-----ARPGT 154

RESULT 7  
 TR14 HUMAN  
 ID TR14 HUMAN STANDARD; PRT; 283 AA.  
 AC Q92956; OSWXR1; Q96J31; Q9UM65;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 14 precursor  
 DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)  
 DE (TR2).  
 GN TNFRSF14 OR HVEM OR HVEA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_Taxid=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cervical adenocarcinoma;  
 RA MEDLINE=97053782; PubMed=8898196;  
 RX Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;  
 RT "Herpes simplex virus-1 entry into cells mediated by a novel member of  
 RL the TNF/NGF receptor family.";  
 RN Cell 87:427-436(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97306336; PubMed=9162061;  
 RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,  
 RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,  
 RA Porter T.G., Truneh A., Young P.R.;  
 RT "A newly identified member of the tumor necrosis factor receptor  
 RT superfamily with a wide tissue distribution and involvement in  
 RT lymphocyte activation";  
 RL J. Biol. Chem. 272:14272-14276(1997).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Wan T., Cao X.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A. AND VARIANTS ARG-17 AND ILE-241.  
 RX MEDLINE=21629477; PubMed=11756979;  
 RA Struyf F., Posavac C.M., Keyaerts E., Van Raest M., Corey L.,  
 RA Spear P.G.;  
 RT "Search for polymorphisms in the genes for herpesvirus entry mediator,  
 RT Nectin-1, and Nectin-2 in immune seronegative individuals.";  
 RL J. Infect. Dis. 185:36-44(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;

RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny N.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Botterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6]  
 RP INTERACTION WITH TRAF2 AND TRAF5.  
 RX MEDLINE=97298041; PubMed=9153189;  
 RA Hsu H., Solovvey I., Colombero A., Elliott R., Kelley M., Boyle W.J.;  
 RT "ATAR, a novel tumor necrosis factor receptor family member, signals  
 RT through TRAF2 and TRAF5.";  
 RL J. Biol. Chem. 272:13471-13474(1997).  
 [7]  
 RP INTERACTION WITH TRAF3 AND TRAF5.  
 RX MEDLINE=97306297; PubMed=9162022;  
 RA Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,  
 RA Ashkenazi A.;  
 RT "Herpesvirus entry mediator, a member of the tumor necrosis factor  
 RT receptor (TNFR) family, interacts with members of the TNFR-associated  
 RT factor family and activates the transcription factors NF-kappaB and  
 RT AP-1.";  
 RL J. Biol. Chem. 272:14029-14032(1997).  
 [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.  
 RX MEDLINE=21403268; PubMed=11511370;  
 RA Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,  
 RA Eisenberg R.J., Wiley D.C.;  
 RT "Herpes simplex virus glycoprotein D bound to the human receptor  
 RT HveA.";  
 RL Mol. Cell 8:169-179(2001).  
 CC -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays  
 CC an important role in HSV pathogenesis because it enhanced the  
 CC entry of several wildtype HSV strains of both serotypes into CHO  
 CC cells, and mediated HSV entry into activated human T cells.  
 CC -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION  
 CC IN LUNG, SPLEEN, AND THYMUS.  
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC  
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 CC  
 CC EMBL; U70321; AAB58354.1; --  
 CC EMBL; U81232; AAD00505.1; --  
 CC EMBL; AF153978; AAF75588.1; --  
 CC EMBL; AF373877; AAL47717.1; --  
 CC EMBL; AF373878; AAL47718.1; --  
 CC EMBL; BC002794; AAH02794.1; --  
 CC PDB; 1JMA; 26-SEP-01.  
 CC Genew; HGNC:11912; TNFRSF14.

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DR MIM; 602746; ..
DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PRO1680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 38
FT CHAIN 39 283
FT DOMAIN 39 202
FT TRANSMEM 203 223
FT DOMAIN 224 283
FT REPEAT 42 75
FT REPEAT 78 119
FT REPEAT 121 162
FT DISULFID 42 53
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 138
FT DISULFID 127 135
FT CARBOHYD 110 110
FT CARBOHYD 173 173
FT VARIANT 17 17
FT VARIANT 241 241
FT TURN 44 45
FT STRAND 46 46
FT STRAND 49 49
FT TURN 50 51
FT STRAND 52 52
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FT STRAND 137 140
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;

Query Match
Best Local Similarity 29.1%; Pred. No. 1.4e-11;
Matches 43; Conservative 26; Mismatches 69; Indels 10; Gaps 3;

QY 1 MVRPLPQCWLWG--CLLTAVHPFPACREKQYVLNSQCCSLCQPGQKLVSDCTFTTTE 58
DQ 20 VLRLVLYLFLGAPCVAPAL-----PSCKEDYVPVGVSECCPKCPGYRVEKAGBELTGTV 74
QY 59 CLPCGSGSEFLDTWNRETHCHQKYCDPNLGLRVQKGTSETDTICTCEGWHC---TSEA 115
DQ 75 CBPCPPTGTHIHLNGSKLCLQCMQCDPAMGLRARNCSRTENAVCCSPGHCFTIVQDGH 134
QY 116 CBSCVLHRSRCSPGFGYKQIAVRPKTWLC 143
DQ 135 CAACRAYATSSPGQRVOKGKTGSDTLG 162
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RESULT 8
TNR3_HUMAN
ID TNR3_HUMAN STANDARD; PRT; 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE protein) (Tumor necrosis factor C receptor).
GN LTR OR TNFSF3 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RA "Construction and evaluation of a hncDNA library of human l2p
RA transcribed sequences derived from a somatic cell hybrid.";
RA Genomics 16:214-218(1993).
RN 2;
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshnyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 3;
RN FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RA "A lymphotoxin-beta-specific receptor.";
RA Science 264:707-710(1994).
RN 4;
RN CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RA death in HeLa cells.";
RA J. Biol. Chem. 274:11868-11873(1999).
RN 5;
RN FUNCTION.
RX MEDLINE=20261554; PubMed=10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RA "The lymphotoxin-beta receptor is necessary and sufficient for
RA LIGHT-mediated apoptosis of tumor cells.";
RA J. Biol. Chem. 275:14307-14315(2000).
RN 6;
RN INTERACTION WITH TRAF3.
```

EX MEDLINE=96278943; PubMed=8663299;  
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
RA Yagita H., Okumura K.;  
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for  
RT the lymphotoxin-beta receptor.";  
RL J. Biol. Chem. 271:14661-14664(1996).  
RN [7]  
RP INTERACTION WITH TRAF4.  
RX MEDLINE=96289299; PubMed=9626059;  
RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,  
RA Gascayne R.D., Bereri K., McFadden D., Shabal A., Hugh J.,  
RA Reynolds A., Cleveland C.V., Reed J.C.;  
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal  
RT adult, fetal, and tumor tissues";  
RL Am. J. Pathol. 152:1549-1561(1998).  
RN [8]  
RP INTERACTION WITH TRAF5.  
RX MEDLINE=9812745; PubMed=9511754;  
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
RA Otsuka M., Yamamoto T., Inoue J.-I.;  
RT "Cloning and characterization of a cDNA encoding the human homolog of  
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
RL Gene 207:135-140(1998).  
RN [9]  
RP FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
RX LTA and LTb, and for TNFbeta/LIGHT. Promotes apoptosis via TRAF3  
RX and TRAF5. May play a role in the development of lymphoid organs.  
CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC DR EMBL; L04270; AAA36757.1; -;  
CC DR EMBL; BC026262; AAH26262.1; -;  
CC DR PIR; I54182; I54182.  
CC DR HSP; P25942; 1CDF.  
CC DR Genew; HGNC:6718; LTBR.  
CC DR MIN; 600979; -;  
CC DR GO; GO:0007165; P:signal transduction; TAS.  
CC DR InterPro; IPR008063; Fas receptor.  
CC DR Pfam; PF00020; TNFR\_c6; 4.  
CC DR PRINTS; PR01680; FASRECEPTOR.  
CC DR SMART; SM00208; TNFR; 4.  
CC DR PROSITE; PS00652; TNFR NGFR\_1; 2.  
CC DR PROSITE; PS00650; TNFR NGFR\_2; 3.  
CC DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
CC SIGNAL 1 30  
CC CHAIN 31 435  
CC FT TUMOR NECROSIS FACTOR RECEPTOR  
CC FT SUPERFAMILY MEMBER 3.  
CC FT EXTRACELLULAR (POTENTIAL).  
CC FT POTENTIAL.  
CC FT TRANSMEM 228 248  
CC FT DOMAIN 249 435  
CC FT REPEAT 42 81  
CC FT REPEAT 82 124  
CC FT REPEAT 125 168  
CC FT REPEAT 169 211  
CC FT BY SIMILARITY.  
CC FT DISULFID 43 58  
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CC FT DISULFID 62 80  
CC FT DISULFID 83 98  
CC FT DISULFID 101 116  
CC FT DISULFID 124 142  
CC FT DISULFID 146 162  
CC FT DISULFID 139 148  
CC FT DISULFID 142 167  
CC FT DISULFID 170 185

FT CARBOHYD 40 40 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 177 177 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;  
Query Match 21.9%; Score 200; DB 1; Length 435;  
Best Local Similarity 36.5%; Pred. No. 3.2e-11;  
Matches 50; Conservative 15; Mismatches 58; Indels 14; Gaps 6;  
QY 5 PLOQVINGCLLTAVHPE--PTTA-----CR--EKQYLINSQ--CCSLCQPOQKVLVSCTE 53  
DB 16 PLVLGLFG-LLAASQPAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYYSAKCSR 74  
QY 54 FTEBCLPGSGSEFLDTWRNTHCHQHKYCDPNLGLRVQOKGTSETTICTCEBGMHCTS 113  
DB 75 IRDIVCATCAENSYNENHNYLITICQLGPCDPVWGLBEIAPCTSKRKTQCRQCFGMCAA 134  
QY 114 EA--CESCVLHRSCLSPG 128  
DB 135 WALECTHCELLSDCPPG 151  
RESULT 9  
TNR6 RAT STANDARD; PRT; 324 AA.  
AC Q63199;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL  
DE receptor) (Apoptosis-mediating surface antigen Fas) (Apo-1 antigen)  
DE (CD95).  
GN TNFRSF6 OR FTL OR FAS.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=94128114; PubMed=7507668;  
RA Kimura K., Yamamoto M., Wakatsuki T.;  
RT "A variant mRNA species encoding a truncated form of Fas antigen in  
RT the rat liver.";  
RL Biochem. Biophys. Res. Commun. 198:666-674(1994).  
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD  
CC recruits caspase-8 to the activated receptor. The resulting death-  
CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
CC activation which initiates the subsequent cascade of caspases  
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
CC mediated apoptosis may have a role in the induction of peripheral  
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
CC both (By similarity).  
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC DR EMBL; D26112; BAA05108.1; -;  
CC DR PIR; JC2395; JC2395.  
CC DR HSP; P25445; 1DDF.  
CC DR InterPro; IPR000488; Death.  
CC DR InterPro; IPR008063; Fas\_receptor.  
CC DR InterPro; IPR001368; TNFR\_c6.

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DR Pfam; PF000531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 324
FT DOMAIN 22 171
FT TRANSMEM 172 188
FT DOMAIN 189 324
FT REPEAT 43 79
FT REPEAT 80 123
FT REPEAT 124 163
FT DOMAIN 219 303
FT DISULFID 44 55
FT DISULFID 56 69
FT DISULFID 59 78
FT DISULFID 81 97
FT DISULFID 100 115
FT DISULFID 103 123
FT DISULFID 125 139
FT DISULFID 142 154
FT CARBOHYD 43 43
FT CARBOHYD 114 114
FT CARBOHYD 132 132
FT CARBOHYD 132 132
SQ SEQUENCE 324 AA; 36835 MW; D2SD583C909D9D09 CRC64;

Query Match 20.6%; Score 188.5; DB 1; Length 324;
Best Local Similarity 30.6%; Pred. No. 2.7e-10;
Matches 44; Conservative 20; Mismatches 69; Indels 11; Gaps 5;

QY 21 EPTACREKQYLINSQCCLCPGOKLYSDC-TEFTECELCPCG-SFELDTWNRTHCH 78
DB 39 EYDNNCEGLYGVGFPCPCPGKRVKDCFTSGGAPTCHEGEBYDRKHVSKCR 98
QY 79 QHKYCDPNLGLRVQKQGTSETDTICTCEGWHCTSEACESCVLHRSCTPGFGVKQI---A 135
DB 99 RCAFCDEGHGLEVEINCTRTQNTKCKENFYCNASLDCDHCYHCTSC---GLEDLLEPC 154
QY 136 VPKTWLCNRQAT--RLMLSVVP 157
DB 155 TRTSNTKCKKQSSNYKLLWLLLP 178

RESULT 10
ID T11B_RAT STANDARD; PRT; 401 AA.
AC 008727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN TNFRSF11B OR OPF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luehry R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Clegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,

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RA Suggs S., Boyle W.J.;
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RL of bone density.";
CC Cell 89:309-319(1997).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Upregulated by osteopontin.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U94330; AAB53707.1; -.
DR HSSP; P25942; 1CDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
SQ SEQUENCE 401 AA; 46192 MW; FEC6A31FIDA573A CRC64;

Query Match 19.8%; Score 181; DB 1; Length 401;
Best Local Similarity 32.3%; Pred. No. 1.6e-09;
Matches 42; Conservative 17; Mismatches 55; Indels 16; Gaps 5;

QY 18 VHPPTACREKQYLINSQCCLCPGOKLYSDC-TEFTECELCPCG-SFELDTWNRTHCH 77
DB 29 LHYDPEPTG---RQLL-----CDKCAPGTYLKQCTVRRKTKLCVPCPDYSYDTSWHTSDEC 80
QY 78 HQHKYCDPNLGL--LRVQKGTSETDTICTCEGWHCTSEACESCVLHRSCTPGFGVKQIA 135
DB 81 ---VYCSFVKCKELQTVKQECNRTNVRVCECEBERYL---ELEFLKXRSCTPGGLVLOAG 134

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QY 136 VRPKWLCNR 145  
DB 135 TPERNVCKR 144

RESULT 11  
TNR6 MOUSE STANDARD; PRT; 327 AA.  
AC P25436, Q9DCQ1; 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
GN TNFRSF6 OR APT1 OR FAS.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92148151; PubMed=1371136;  
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S., Copeland N.G., Jenkins N.A., Nagata S.;  
RT "The cDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.";  
RL J. Immunol. 148:1274-1279(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129/SV;  
RA Koczan D., Ibrahim S.M., Thiesen H.J.;  
RT "Role of a mutant fas receptor in a transgenic mouse.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gisi C., King B., Kochiwa H., Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [4]  
RP SEQUENCE OF 1-96 FROM N.A.  
RX MEDLINE=93189576; PubMed=7680478;  
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;  
RT "Aberrant transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr mice.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).  
RN [5]  
RP INTERACTION WITH DAXX.  
RX MEDLINE=97358533; PubMed=9215629;  
RA Yang X., Khosravi-Far R., Chang H.Y., Baltimore D.;  
RT "Daxx, a novel Fas-binding protein that activates JNK and apoptosis.";  
RL Cell 89:1067-1076(1997).  
RN [6]

RP VARIANT LPR.  
RX MEDLINE=92195401; PubMed=1372394;  
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A., Nagata S.;  
RT "Lymphoproliferation disorder in mice explained by defects in Fas antigen that mediates apoptosis.";  
RL Nature 356:314-317(1992).  
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).  
CC -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS, LIVER, LUNG, HEART, AND ADULT OVARY.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- DISEASE: Defects in TNFRSF6 are the cause of the lymphoproliferation phenotype (lpr). Lpr mice show lymphadenopathy and autoantibody production.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
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CC  
CC EMBL; M83649; AAA37593.1; -;  
CC EMBL; AK002590; BAB2211.1; -;  
CC EMBL; AJ295702; CAC00638.1; -;  
CC EMBL; AJ295703; CAC00638.1; JOINED.  
CC EMBL; AJ295704; CAC00638.1; JOINED.  
CC EMBL; S56490; AAB25700.1; -;  
CC EMBL; S56485; AAB25700.1; JOINED.  
CC EMBL; S56486; AAB25700.1; JOINED.  
CC PIR; A46484; A46484.  
CC HSP; P25445; 1DDF.  
CC MGD; MGI:95484; Tnfrsf6.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR008063; Fas\_receptor.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00020; TNFR\_c6; 3.  
CC PRINTS; PR01580; FASRECEPTOR.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00208; TNFR; 3.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
CC PROSITE; PS0017; DEATH\_DOMAIN; 1.  
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
KW Disease mutation.  
FT SIGNAL 1 21  
FT CHAIN 22 327  
FT FT  
FT DOMAIN 22 169 TUMOR NECROSIS FACTOR RECEPTOR  
FT TRANSMEM 170 186 SUPERFAMILY MEMBER 6.  
FT DOMAIN 187 327 EXTRACELLULAR (POTENTIAL).  
FT REPEAT 43 79 POTENTIAL.  
FT REPEAT 80 123 CYTOSOLIC (POTENTIAL).  
FT REPEAT 124 162 TNFR-CYS 1.  
FT REPEAT 162 306 TNFR-CYS 2.  
FT DOMAIN 222 306 TNFR-CYS 3.  
FT DISULFID 44 55 DEATH.  
FT DISULFID 56 69 BY SIMILARITY.  
FT DISULFID 59 78 BY SIMILARITY.  
FT DISULFID 81 97 BY SIMILARITY.

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FT DISULFID 100 115 BY SIMILARITY.
FT DISULFID 103 123 BY SIMILARITY.
FT DISULFID 125 139 BY SIMILARITY.
FT DISULFID 142 153 BY SIMILARITY.
FT DISULFID 145 161 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 I -> N (IN LPR). 3).
FT CONFLICT 38 38 H -> R (IN REF. 3).
SQ SEQUENCE 327 AA; 37418 NW; F6BFFC5ACE356EEE CRC64;

Query Match
Best Local Similarity 33.6%; Pred. No. 1.6e-09;
Matches 49; Conservative 15; Mismatches 68; Indels 14; Gaps 6;

QY 18 VPEPPTACREKQYLINSQCCLQPGQKLVSDDCTETET-BCLPCGB-SFELDTWNET 75
Db 37 VH-ETDKNKGSEGLYGGFFCCQPCQFGKKKVEDCKWNGGTFTCAPCTGKGYMDKNHYAD 95
QY 76 HCHOHKYCDPNGLRVOQKGTSETDTICTCEGHWCTSEACESCVLHRSCTPGFGVKQIA 135
Db 96 KCRRTCLDDEHGLEVETNCTITQNTKCKKDFDCDPSGCEHCVRCSCEHG-----T 149
QY 136 VPKPTWL-----CNROA-QTRMLSLV 156
Db 150 LEPCTATNTNCRKQSPRNLWLTII 175

RESULT 12
TI1B HUMAN
ID TI1B HUMAN STANDARD; PRT; 401 AA.
AC O00300; C60236; Q9UHP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11b precursor
DE (osteoprotegerin) (osteoclastogenesis inhibitory factor).
GN TNFRSF11B OR OPG OR OCIF.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wondan S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RL Cell 89:309-319(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung cancer;
RX MEDLINE=98151033; PubMed=9492069;
RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA Tsuda E., Morinaga T., Higashio K.;
RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT osteoclastogenesis in vitro.";
RN Endocrinology 139:1329-1337(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Placenta;
RX MEDLINE=98351569; PubMed=9688283;
RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT "Cloning and characterization of the gene encoding human
RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC TISSUE=Eye;
RX MEDLINE=98238257; PubMed=9603945;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Saplaton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RN Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN [6]
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RX He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RN Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN [7]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis.";
RN Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN [8]
RP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RN J. Biol. Chem. 273:14363-14367(1998).
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor.";
RN J. Biol. Chem. 273:5117-5123(1998).
RN [10]
RP REVIEW.
RX MEDLINE=21395914; PubMed=11505389;
RA Hofbauer L.C., Neuberger A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases.";
RL Cancer 92:460-470(2001).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
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its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta, and in embryo.

CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal aorta and midgut.

CC -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by 1,25-dihydroxyvitamin D3 and parathyroid hormone.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- SIMILARITY: Contains 2 death domains.

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CC -----

DR EMBL; U94331; AAB53708.1; --

DR EMBL; AB013898; BAA28269.1; --

DR EMBL; AB013903; BAA33388.1; --

DR EMBL; AB013899; BAA33388.1; JOINED.

DR EMBL; AB013900; BAA33388.1; JOINED.

DR EMBL; AB013901; BAA33388.1; JOINED.

DR EMBL; AB013902; BAA33388.1; JOINED.

DR HSSP; P25942; 1CDF.

DR GGD; MG1:09587; Tnfrcfl1b.

DR GO; GO:0005578; C:extracellular matrix; IDA.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001368; TNFR NGFR.2; 2.

DR Pfam; PF00020; TNFR\_c6; 3.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00017; DEATH\_DOMAIN; 1.

DR PROSITE; PS00652; TNFR NGFR.1; 1.

DR PROSITE; PS00050; TNFR NGFR.2; 2.

DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.

KW SIGNAL 1 21 BY SIMILARITY.

FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR

FT REPEAT 24 62 SUPERFAMILY MEMBER 11B.

FT REPEAT 65 105 TNFR-CYS 1.

FT REPEAT 107 142 TNFR-CYS 3.

FT REPEAT 145 185 TNFR-CYS 4.

FT DOMAIN 198 269 DEATH 1.

FT DOMAIN 283 365 DEATH 2.

FT SITE 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).

FT DISULFID 41 54 BY SIMILARITY.

FT DISULFID 44 62 BY SIMILARITY.

FT DISULFID 65 80 BY SIMILARITY.

FT DISULFID 83 97 BY SIMILARITY.

FT DISULFID 87 105 BY SIMILARITY.

FT DISULFID 107 118 BY SIMILARITY.

FT DISULFID 124 142 BY SIMILARITY.

FT DISULFID 145 160 BY SIMILARITY.

FT DISULFID 166 185 BY SIMILARITY.

FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).

FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).

FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 19.2%; Score 175; DB 1; Length 401;

Best Local Similarity 30.0%; Pred. No. 5.7e-09;

Matches 39; Conservative 18; Mismatches 57; Indels 16; Gaps 4;

QY 18 VHPPEPTACREKQYLINSQCCLCPQCKLVSDCTETETETCLPQGESEFLDTWNRTHC 77

Db 29 LHYDPEITG-----HOLLCDKCAPGTLYLKQHTKLVCPDPHSYTDSWHTSDEC 80

QY 78 HQHKYCDPNLG--LRVQOKGTSETDICTCEGHWHCTSEACESCVLHRSCTPGYKQIA 135

Db 81 ---VYCSFVCKELQSVKQECNTRNRYCECEGRYL---EIFCLKHRSCPPGSGVVOAG 134

QY 136 VRPKTWLCNR 145

Db 135 TPERNTVCKK 144

RESULT 14

TR1B MOUSE

ID TR1B MOUSE STANDARD; PRT; 474 AA.

AC P25119; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (p75).

GN TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."

RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).

RN [2] SEQUENCE FROM N.A.

RP MEDLINE=91246168; PubMed=1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."

RT Mol. Cell. Biol. 11:3020-3026 (1991).

RN [3] SEQUENCE OF 1-26 FROM N.A.

RP STRAIN=NOD;

RA Jacob C.O., Liu J.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4] SEQUENCE OF 1-22 FROM N.A.

RP TISSUE=Liver;

RA Kissinger M., Fellows R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By similarity).





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 21, 2004, 10:03:04 ; Search time 39 Seconds  
(without alignments)  
1294.434 Million cell updates/sec

Title: US-10-031-607-7  
Perfect score: 913  
Sequence: 1 MVRPLQCVLWGCLLTAVHP.....WLCNRQAQTRMLSVVRIG 160

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organalle.\*  
9: sp\_phage.\*  
10: sp\_plan.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	785	86.0	223	4	Q85YK5
2	615	67.4	278	6	Q8SQ34
3	588	62.2	274	6	Q7YRL5
4	563	61.7	277	6	Q8WMQ2
5	477	52.2	289	11	Q8K2X6
6	463	50.7	169	11	Q9JKE0
7	296	32.4	276	13	Q9DD22
8	229.5	25.1	275	11	Q8QWM9
9	196.5	21.5	283	6	Q9XSZ8
10	180	19.7	146	13	Q900K7
11	180	19.7	150	11	Q7ZZY4
12	180	19.7	150	11	Q9R230
13	176.5	19.3	462	13	Q8Q5B0
14	174.5	19.1	459	11	Q62327
15	170.5	18.7	328	6	Q9BDP0
16	170	18.6	349	12	O57111

17	170	18.6	349	12	O57110
18	170	18.6	349	12	Q8QSR3
19	169	18.5	348	12	O57108
20	169	18.5	348	12	O57277
21	169	18.5	348	12	O57103
22	169	18.5	349	12	O57101
23	168.5	18.5	263	6	Q9XS60
24	168.5	18.5	319	6	Q9TV79
25	168.5	18.5	320	6	Q9XS29
26	168	18.4	331	6	Q9GK36
27	168	18.4	349	12	O57098
28	168	18.4	349	12	O57284
29	167.5	18.3	348	12	O57112
30	167	18.3	318	13	Q7TZH3
31	166	18.2	331	6	Q9BDN0
32	166	18.2	331	6	Q9BDN4
33	166	18.2	331	6	Q9TSN4
34	166	18.2	349	12	O57100
35	166	18.2	349	12	O57102
36	166	18.2	349	12	O57291
37	165	18.1	474	11	Q8QW16
38	164	18.0	333	6	Q9BDP2
39	164	18.0	349	12	O57099
40	163.5	17.9	482	11	O88734
41	162.5	17.8	314	6	Q861W6
42	162.5	17.8	334	6	Q9GL40
43	162	17.7	349	12	O57109
44	162	17.7	349	12	O57097
45	162	17.7	349	12	O57305

ALIGNMENTS

RESULT 1

Q86YK5 PRELIMINARY; PRT; 223 AA.  
AC O86YK5  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE -Tumor necrosis factor receptor superfamily member 5 (Fragment).  
GN TNFRSF5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA He X., Xu L., Zeng Y.;  
RT "Transcripts of CD40 isoform in peripheral mononuclear cells.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY225405; AAC43990.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0006955; P:apoptosis; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR GO; GO:0007155; P:signal transduction; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR008063; Fas\_receptor.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR PRINTS; PR01680; FASRECEPTOR.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
DR Receptor.

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FT NON TER 223 223
SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 86.0%; Score 785; DB 4; Length 223;
Best Local Similarity 95.1%; Pred. No. 1.3e-81;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSOCSCLOPQKLVSDCTEFTETEC 60
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSOCSCLOPQKLVSDCTEFTETEC 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
QY 121 LHRSCSPGFGVKQIAPKPTWLC 143
DB 121 LHRSCSPGFGVKQIATGVSDTIC 143

RESULT 2
Q8SQ34 PRELIMINARY; PRT; 278 AA.
AC Q8SQ34;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RT "Characterization of the Porcine CD40 Molecule.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF248545; AAL92924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 4.
SQ SEQUENCE 278 AA; 30551 MW; 20D446B44AF93DD2 CRC64;

Query Match 67.4%; Score 615; DB 6; Length 278;
Best Local Similarity 71.3%; Pred. No. 4.6e-62;
Matches 102; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSOCSCLOPQKLVSDCTEFTETEC 60
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYPTNSCCNCPGQKLVNHCTEVTETEC 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
DB 61 PCSSEFLATWNRKCHQHKYCDPNLGLVQREGTSKDTTTCVSEGHCTNSACESCT 120
QY 121 LHRSCSPGFGVKQIAPKPTWLC 143
DB 121 LHSCLPPLGLVKOMATEVSDTIC 143

RESULT 3
Q7YRL5 PRELIMINARY; PRT; 274 AA.
ID Q7YRL5;
AC Q7YRL5;

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD40.
GN CD40.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Sim G.-K.;
RT "Canine CD40 and CD40 Ligand cDNA Sequences.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333789; AAP86653.1; -.
SQ SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;

Query Match 62.2%; Score 568; DB 6; Length 274;
Best Local Similarity 65.3%; Pred. No. 1.1e-56;
Matches 94; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSOCSCLOPQKLVSDCTEFTETEC 60
DB 1 MVLPLRCLFWGSLTIVPEPTACREKQYLVDSQCNCMPGKRLVNDLHTIDTECT 60
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120
DB 61 RCQTGEFLDTWNAERHCHQHKYCDPNLGLHVEKGTSETDTTCTCDSGLCTNAACESCT 120
QY 121 LHRSCSPGFGVKQIAPKPTWLCN 144
DB 121 MHSCLPPGLGVKQIATGISTIDC 144

RESULT 4
Q8WNQ2 PRELIMINARY; PRT; 277 AA.
ID Q8WNQ2;
AC Q8WNQ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Membrane protein CD40 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Zawitkowski M.S., Russ G.R., Krishnan R.;
RT "Cloning and expression of the ovine CD40 molecule and the inhibition of the mixed lymphocyte reaction by the ovine CD40-EGFP fusion protein.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072798; AAL68402.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
FT NON TER 277
SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

Query Match 61.7%; Score 563; DB 6; Length 277;
Best Local Similarity 65.7%; Pred. No. 4e-56;
Matches 94; Conservative 15; Mismatches 34; Indels 0; Gaps 0;

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QY 1 MYRLPQCVLWGLLTAVHPPEPTACREKQYLINSQCSLCPGQKLVSDCTETETECL 60
D 1 MYRLPQCVLWGLLTAVHPPEPTACREKQYLINSQCSLCPGQKLVSDCTETETECL 60
QY 61 PGSESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTCTCEEGHCTSEACSCV 120
D 61 SCGGEFLSTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTCTCEEGHCTSEACSCV 120
QY 121 LHRSCSPGFVGVKQIAVRPKTWLC 143
D 121 PHSLLCLPGFVGVKQIAVRPKTWLC 143

RESULT 5
Q8K2X6 PRELIMINARY; PRT; 289 AA.
AC Q8K2X6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029254; AAH29254.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007155; P:signal transduction; IEA.
DR InterPro; IPR008063; FAS_receptor.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 289 AA; 32077 MW; DBE93BLE439F1E2A CRC64;

Query Match 52.2%; Score 477; DB 11; Length 289;
Best Local Similarity 54.2%; Pred. No. 2.9e-46;
Matches 78; Conservative 21; Mismatches 45; Indels 0; Gaps 0;

QY 1 MYRLPQCVLWGLLTAVHPPEPTACREKQYLINSQCSLCPGQKLVSDCTETETECL 60
D 1 MYRLPQCVLWGLLTAVHPPEPTACREKQYLINSQCSLCPGQKLVSDCTETETECL 60
QY 61 PGSESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTCTCEEGHCTSEACSCV 120
D 61 SCGGEFLSTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTCTCEEGHCTSEACSCV 120
QY 121 LHRSCSPGFVGVKQIAVRPKTWLC 144
D 121 QHTPCIPGFGVGMETATETDTVCH 144

RESULT 6
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Q9JKE0 PRELIMINARY; PRT; 169 AA.
AC Q9JKE0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CD40 protein (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE OF 62-169 FROM N.A.
RA STRAIN=Wistar; TISSUE=Smooth muscle;
RX MEDLINE=9330195; Pubmed=10403401;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
RT cells is mediated by nuclear factor kappaB and signal transducer and
RT activator of transcription-1."
RL FEBS Lett. 453:191-196(1999).
RN [2]_
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Smooth muscle;
RX Krzesz R., Hecker M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]_
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Smooth muscle;
RX Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241231; AAF43717.2; -
DR HSSP; Q92956; LOMA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0007155; P:signal transduction; IEA.
DR InterPro; IPR008063; FAS_receptor.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
DR NON TER 169
FT SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;

Query Match 50.7%; Score 463; DB 11; Length 169;
Best Local Similarity 53.1%; Pred. No. 6.5e-45;
Matches 76; Conservative 21; Mismatches 46; Indels 0; Gaps 0;

QY 1 MYRLPQCVLWGLLTAVHPPEPTACREKQYLINSQCSLCPGQKLVSDCTETETECL 60
D 1 MYRLPQCVLWGLLTAVHPPEPTACREKQYLINSQCSLCPGQKLVSDCTETETECL 60
QY 61 PGSESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTCTCEEGHCTSEACSCV 120
D 61 PCDSGEFSAHWNREIRCHQHRCEPQGLRVKKEGTAESDTCVCKEGHCTSEACSCV 120
QY 121 LHRSCSPGFVGVKQIAVRPKTWLC 143
D 121 QHRPCGFGVGVQVATETDTVC 143

RESULT 7
Q9DDD2 PRELIMINARY; PRT; 276 AA.
ID Q9DDD2
```

AC Q9DD2; 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Human CD40-homologue.  
 GN TNFSF5.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tregaskes C.A., University of Reading, Reading, UNITED KINGDOM.  
 RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.  
 DR EMBL; AJ293700; CAC20218.1; -.  
 DR HSSP; Q92956; 1JMA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004988; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008063; F: Fas receptor.  
 DR InterPro; IPR001005; Myb DNA binding.  
 DR Pfam; PF00020; TNFR\_c6.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00037; MYB\_1; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

Query Match 32.4%; Score 296; DB 13; Length 276;  
 Best Local Similarity 37.7%; Pred. No. 1.3e-25;  
 Matches 49; Conservative 25; Mismatches 56; Indels 0; Gaps 0;

QY 1 MVRPLQVLWGCLLTAVHPPTACREKQYLINSQCCLQCPGQKLVSDCTETETECLE 60  
 DB 1 MGRLLGLLICALLCGGCGDGVNSDKQYEHKGRCCRCQPEKLAECNDTEBSVCT 60  
 QY 61 PQSESEFLDWNRETHCHQHKYCDPNGLRVQOKGTSETDTICTCEGWHCTSE--ACSCVLHRS 120  
 DB 61 PCENGQYQHSWTKERHCTHEICEDNAGLIVKRGHNATHNTVQCQAGNHCSDASQTCV 120  
 QY 121 LHRSCSPGFG 130  
 DB 121 ENEPCKQGGF 130

RESULT 8  
 Q8QW9 PRELIMINARY; PRT; 275 AA.  
 AC Q8QW9  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 14 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6; TISSUE=Thymus;  
 RC Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;  
 RT "Light regulation in a murine model of ovarian carcinoma."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY264405; AA089081.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008063; Fas receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SMO0208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Signal.  
 FT SIGNAL 1 38 Potential.  
 SQ SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;

Query Match 25.1%; Score 229.5; DB 11; Length 275;  
 Best Local Similarity 30.9%; Pred. No. 5.4e-18;  
 Matches 43; Conservative 29; Mismatches 62; Indels 5; Gaps 2;

QY 8 CVLWGCLLTAVHPPTACREKQYLINSQCCLQCPGQKLVSDCTETETECLEPCGESEF 67  
 DB 26 CVFLNLLQRIASQP--SCQEEFLVGDCCPMCPNPGYHVKQVSEHTGIVCAPCPQTY 83  
 QY 68 LDTWNRETHCHQHKYCDPNGLRVQOKGTSETDTICTCEGWHCTSE---ACSCVLHRS 124  
 DB 84 TAHANGLSKCLPCGVCDPDMGLLTWQBCSSWKDVCRCIPGYFCENQDGHSCSTCLOHTT 143  
 QY 125 CSPGPGVKQIAVRPKTWLC 143  
 DB 144 CPGQVEXRGTHDQDVC 162

RESULT 9  
 Q9XS28 PRELIMINARY; PRT; 283 AA.  
 ID Q9XS28  
 AC Q9XS28  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE HVEAS.  
 GN HVEAS.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=95296730; PubMed=10366573;  
 RA Foster T.P., Chouljenko V.N., Kousoulas K.G.;  
 RT "Functional characterization of the HveA homolog specified by African  
 RT green monkey kidney cells with a herpes simplex virus expressing the  
 RT green fluorescence protein.";  
 RL Virology 258:365-374(1999).  
 DR EMBL; AF147720; AAD37381.1; -.  
 DR HSSP; Q92956; 1JMA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008063; Fas receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR PRINTS; PR01680; FASRECEPTOR.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 21.5%; Score 196.5; DB 6; Length 283;  
 Best Local Similarity 30.3%; Pred. No. 3.3e-14;  
 Matches 37; Conservative 24; Mismatches 58; Indels 3; Gaps 1;

```
QY 25 ACREKQYVINSQCSLQCPGQKLVSDCTFTETETCLPGSESEFLDTWNRTHCHQKXCD 84
DB 41 SKDEBYVPGSCCKPGFHVROACGEQGTVCPCSPGTYYAHFNLGSKLQCCQMC 100
QY 85 PNLGLRVQKGTSETDTTCTCEGWHC---TSEACESCVLHRSQSPGFGVKQIAPVPTX 141
DB 101 PAKGLRTSNCSTTANALCGSPGHFCLIQGDHCAACRAVATSPGQVQKGTESQDT 160
QY 142 LC 143
DB 161 LC 162

RESULT 10
Q800K7 PRELIMINARY; PRT; 483 AA.
AC Q800K7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-2.
GN TNFR_2.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthysidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Kurobe T., Hirano I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
RT factor receptor superfamily genes from Japanese flounder Paralicthys
RT olivaceus."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080947; BAC65226.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64;

Query Match 21.5%; Score 196.5; DB 13; Length 483;
Best Local Similarity 30.6%; Pred. No. 5.7e-14;
Matches 41; Conservative 19; Mismatches 65; Indels 9; Gaps 3;

QY 4 LPQCVLWGLLTAVHPBPPTACREK--QYLINSQCSLQCPGQKLVSDCTFTETCLP 61
DB 8 LLLLCVR---TTAYRLSDSGKHNSTTEYRQDLCKCKCPGQRLQKCSATESVCKQ 64
QY 62 CGSESEFLDTWNRTHCHQKXCDPNLGLRVQKGTSETDTTCTCEGWHCTSE---ACE 117
DB 65 CDSGQVNEKYNKAAQKCLCNKCKSNKGLQYAGRCSTTITGVCVCKPGNVCINDFNPYCA 124
QY 118 SCVLHRSQSPGFGV 131
DB 125 ECRNYSQCRAGYGV 138

RESULT 11
Q72ZY4 PRELIMINARY; PRT; 146 AA.
AC Q72ZY4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Osteoprotegerin (fragment).
GN OPG.
OS Gallus gallus (Chicken).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "Osteoprotegerin (OPG) expression in the hen ovary."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251407; AAP03890.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
FT NON TER 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9B64FE3A0FC2DF CRC64;

Query Match 19.7%; Score 180; DB 13; Length 146;
Best Local Similarity 30.5%; Pred. No. 1.3e-12;
Matches 39; Conservative 19; Mismatches 54; Indels 16; Gaps 5;

QY 18 VHPBPPTACREKQYVINSQCSLQCPGQKLVSDCTFTETETCLPGSESEFLDTWNRTHC 77
DB 29 LHVDPGTS---RQVM-----CNQPPGYSYVKQHCCTAASPTVCAPCPDQYVAEDWNSDEC 80
QY 78 HQHKYCDPNLG--LRVQKGTSETDTTCTCEGWHCTSEACESCVLHRSQSPGFGVKQIA 135
DB 81 --QYCAVCKELQYIKQCTSTQDRVCEIEGNYL---ELEFLCKHTECPGFGVAQPG 134
QY 136 VRPKTWLC 143
DB 135 TPESDTVC 142

RESULT 12
Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Corpus luteum;
RA Lareu R.R., Dharmarajan A.;
RT "Cloning and expression of Fas and Fas Ligand in the apoptotic rat
RT corpus luteum."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD20221.1; -.
DR HSSP; Q92956; LUNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER 1 1
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```
FT NON TER 150 150
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 19.7%; Score 180; DB 11; Length 150;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 36; Conservative 14; Mismatches 55; Indels 2; Gaps 2;

QY 21 EPTACREKQYLNSQCCSLQCPQKLVSDC-TFTETECPLPQCE-SEFLDTWNRTHCH 78
DB 34 ETDNNCEGLYQVGFCCQCPQGERKVKDCTTSGAPTCHPCTGEBY*DRXHSKCR 93
QY 79 QHKYCDNGLRVQKGTSETDTICTCEGWHCTSEACESCVLHRS 125
DB 94 RCAFCDHGHEVETNCTRTQNTKCRCKENFYCNASLCDHCYHCTSC 140

RESULT 13
Q805B0 PRELIMINARY; PRT; 462 AA.
AC Q805B0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-II.
GN TNFR-II.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayde A.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayed A., Horuchi H., Furusawa S., Matsuda H.;
RT "Molecular cloning and characterization of chicken Tumor necrosis
RT factor receptor-II (TNFR-II) and tumor necrosis factor receptor
RT associated factor-5 (TRAF-5) genes.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101004; BAC55966.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR Pfam; PF00020; TNFR_C6; 3.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match 19.3%; Score 176.5; DB 13; Length 462;
Best Local Similarity 30.8%; Pred. No. 1e-11;
Matches 36; Conservative 16; Mismatches 54; Indels 11; Gaps 4;

QY 22 PPTACREKQYLNSQCCSLQCPQKLVSDC-TFTETECPLPQCESEFLDTWNRTHCHQHK 91
DB 34 PSTEFYERL---KKCCSKCPGQRKAESCSHSDTKICPLDPTVTAVNRSPOCFA-- 88
QY 82 YCDP--NLGLRVQKGTSETDTICTCEGWHCTSC---EACESCVLHRSCTPGFYKQ 133
DB 89 -CSPPCKKGFVENQTCFLSWDRICSPPNFYCKMYQNCHICKVKKCGRGYRVS 144

RESULT 14
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Q62327
ID Q62327 PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR PIR; I48854; I48854.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0008220; P:necrosis; IMP.
DR InterPro; IPR001368; TNFR_C6; 4.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 1 87
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 19.1%; Score 174.5; DB 11; Length 459;
Best Local Similarity 29.9%; Pred. No. 1.8e-11;
Matches 41; Conservative 20; Mismatches 59; Indels 17; Gaps 6;

QY 4 LPLQCVLWGCLLTAVHREPPPTACREKQYLIN---SQCCSLQCPQKLVSDCTETETEC 60
DB 8 VPAQVW-----LTPYKPEPGVEYECQISOEYDRKAKMCCAKCPGQYKHFNCNTSDTVCA 62
QY 61 PCGESEFLDTWNRTHCHQHKYCDNGLGL-RVQKQK-TSETDTICTCEGWHCT-----SE 114
DB 63 DCEASWYTVQVNWQPTCLS---CSSSCSTDQVETRACTKQNRVCAACEAGRYCALKTHSG 119
QY 115 ACESCVLHRSCTPGFV 131
DB 120 SCRCMLSLKCGPGFV 136

RESULT 15
Q9BDP0 PRELIMINARY; PRT; 328 AA.
ID Q9BDP0
AC Q9BDP0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FAS antigen CD95.
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Job time : 40 secs



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OS Homo sapiens.  
 XX WO2000066155-A1.  
 XX PD 09-NOV-2000.  
 XX PF 28-APR-2000; 2000WO-US011734.  
 XX PR 30-APR-1999; 99US-0131730P.  
 XX PA (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.  
 XX PI Sarawar SR, Schoenberger SP;  
 XX WI; 2001-024740/03.  
 XX Method for preventing latent virus reactivation or controlling virus  
 PT replication by administration of antibodies or similar reagents which  
 PT stimulate the CD40 molecule.  
 XX PS Disclosure; Page 18; 36pp; English.  
 XX CC The present sequence is human CD40. It may be used in a method for  
 CC preventing latent virus reactivation or controlling virus replication.  
 CC The method comprises administering a composition capable of binding to a  
 CC cell membrane expressed CD40, where the binding of the composition to the  
 CC CD40 on the surface of the cell generates a stimulatory signal to the  
 CC cell. The method is useful for treating immunocompromised patients, e.g.  
 CC infected with human immunodeficiency virus (HIV), or immunosuppressed  
 CC patients, e.g. due to infections or illness, or as a side effect of  
 CC treatments (such as radiation or cancer therapy), or due to tissue or  
 CC organ transplantation. The method does not have the levels of toxicity  
 CC seen following administration of conventional antiviral drugs  
 XX SQ Sequence 277 AA;  
 Query Match 86.0%; Score 785; DB 4; Length 277;  
 Best Local Similarity 95.1%; Pred. No. 4e-58;  
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLYNSQCSLCPQKLVSDCTFTETEC 60  
 Db 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLYNSQCSLCPQKLVSDCTFTETEC 60  
 QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDICTCEGWHCTSEACESC 120  
 Db 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDICTCEGWHCTSEACESC 120  
 QY 121 LHRSCSPGFGVKQIATVPRKWTWLC 143  
 Db 121 LHRSCSPGFGVKQIATVPRKWTWLC 143  
 RESULT 15  
 AAB50520  
 ID AAB50520 standard; protein; 277 AA.  
 XX AC AAB50520;  
 XX DT 15-MAR-2001 (first entry)  
 XX DE Human tumour necrosis factor receptor CD40 protein SEQ ID NO:10.  
 XX KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neurotropic;  
 KW TRAIL receptor without intracellular domain; diagnosis; cytosolic;  
 KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
 KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
 KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
 KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
 KW apoptotic cell death related disease; autoimmune disorder;  
 KW cardiovascular disorder; viral infection.  
 XX OS Homo sapiens.

XX WO2000071150-A1.  
 XX 30-NOV-2000.  
 XX 18-MAY-2000; 2000WO-US013515.  
 XX 20-MAY-1999; 99US-0135164P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Wei Y, Ruben SM, Gentz RL, Ni J;  
 XX WI; 2001-041051/05.  
 XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
 PT prevention of cancer, autoimmune disorders and viral infection.  
 XX PS Disclosure; Fig 2; 285pp; English.  
 XX CC The present invention describes the human TRID protein (tumour necrosis  
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
 CC intracellular domain, also referred to as tumour necrosis factor receptor  
 CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, neurotropic,  
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
 CC activities, and can be used in gene therapy. The TRID polynucleotides are  
 CC useful for detecting complementary polynucleotides. TRID proteins and  
 CC polynucleotides are useful in the treatment of tumours, resistance to  
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
 CC They are also useful for inducing proliferation of T-cells, endothelial  
 CC cells and certain haematopoietic cells, to regulate antiviral responses  
 CC and to prevent certain autoimmune diseases after stimulation of TRID by  
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
 CC polypeptides are useful for treating and/or preventing diseases  
 CC associated with increased or decreased apoptotic cell death. The TRID  
 CC polynucleotides, proteins, antibodies, agonists and antagonists are  
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)  
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;  
 CC (d) cardiovascular disorders; and (e) viral infection. The present  
 CC sequence represents a tumour necrosis factor receptor used in comparison  
 CC with TRID in the exemplification of the present invention  
 XX SQ Sequence 277 AA;  
 Query Match 86.0%; Score 785; DB 4; Length 277;  
 Best Local Similarity 95.1%; Pred. No. 4e-58;  
 Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLYNSQCSLCPQKLVSDCTFTETEC 60  
 Db 1 MYRLPQCVLWGCLLTAVHPPTACREKQYLYNSQCSLCPQKLVSDCTFTETEC 60  
 QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDICTCEGWHCTSEACESC 120  
 Db 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDICTCEGWHCTSEACESC 120  
 QY 121 LHRSCSPGFGVKQIATVPRKWTWLC 143  
 Db 121 LHRSCSPGFGVKQIATVPRKWTWLC 143

Search completed: July 21, 2004, 10:05:36  
 Job time : 56 secs

KW nucleotide sequence-based technology; antisense drug discovery.

XX OS Homo sapiens.  
XX PN WO9953101-A1.  
XX PD 21-OCT-1999.  
XX PF 13-APR-1999; 99WO-US008268.  
XX PR 13-APR-1998; 98US-0081483P.  
XX PR 28-APR-1998; 98US-00067638.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasnor HM, Brooks DG;  
XX PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;  
XX DR WPI; 1999-620446/53.  
XX DR N-PSDB; AA240936.  
XX PT Identifying compounds which modulate expression of nucleic acids, used to  
XX PT provide compounds having defined physical, chemical or bioactive  
XX PT properties, e.g. antisense activity.  
XX PS Example 1; Page 177-179; 264pp; English.  
XX CC A method has been developed of defining a set of compounds that modulate  
XX CC the expression of a target nucleic acid (tNA) sequence via binding of the  
XX CC compounds with the tNA sequence. The method comprises generating a  
XX CC library of virtual compounds in silico according to defined criteria, and  
XX CC evaluating in silico the binding of the virtual compounds with the tNA  
XX CC according to defined criteria. Also described are: (1) a method of  
XX CC defining a set of oligonucleotides (ONS) that modulate the expression of  
XX CC a tNA sequence via binding of the ONS with the tNA sequence comprising  
XX CC generating a library of virtual compounds in silico according to defined  
XX CC criteria, and evaluating in silico the binding of the virtual ONS with  
XX CC the tNA according to defined criteria; and (2) a method of defining a set  
XX CC of compounds that modulate the expression of a tNA sequence via binding  
XX CC of the compounds with the tNA. The methods can be used for the generation  
XX CC and identification of synthetic compounds having defined physical, chemical  
XX CC or bioactive properties. Information gathered from assays of  
XX CC such compounds is used to identify nucleic acid sequences that are  
XX CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
XX CC antisense drug discovery and target validation. AA240852 to AA241220, and  
XX CC AA52701 to AA52706, represent sequences used in the exemplification of  
XX CC the present invention

XX SQ Sequence 277 AA;  
Query Match 86.0%; Score 785; DB 2; Length 277;  
Best Local Similarity 95.1%; Pred. No. 4e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MVRLPQCVMGCLLTAVHPEPTACREKQYLINSQCCSLCOPGQKLVSDCTEFTETECCL 60  
DB 1 MVRLPQCVMGCLLTAVHPEPTACREKQYLINSQCCSLCOPGQKLVSDCTEFTETECCL 60  
QY 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
DB 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
QY 121 LHRSCSPGFGVKQIARPKTWLC 143  
DB 121 LHRSCSPGFGVKQIATGVSDTIC 143  
RESULT 13  
AAB84892  
ID AAB84892 standard; protein; 277 AA.  
XX AC AAB84892;  
XX KW human immunodeficiency virus; HIV; cancer; organ transplantation.

DT 03-AUG-2001 (first entry)

XX DE Human CD40 antigen.  
XX KW Human; CD40; immunosuppressive; B cell; autoimmune disease;  
XX KW cell-mediated disease; antibody-mediated disease.

OS Homo sapiens.  
XX PN WO200130974-A2.  
XX PD 03-MAY-2001.

XX PF 25-OCT-2000; 2000WO-US041532.  
XX PR 25-OCT-1999; 99US-0161281P.  
XX PA (TANO-) TANOX INC.

XX PI Chang N;

XX DR WPI; 2001-308629/32.

XX PT Novel CD40-binding non-antibody molecule, that do not cause  
XX PT proliferation, differentiation or activation of CD40-expressing cells but  
XX PT which inhibit CD40 ligand-induced activation, used to treat autoimmune  
XX PT disease.  
XX PS Disclosure; Page 18-19; 19pp; English.

XX CC The present invention relates to non-antibody molecules which bind to an  
XX CC epitope on CD40 antigen and do not activate CD40-expressing cells, but  
XX CC inhibit CD40-ligand (CD40L) induced activation, and which do not  
XX CC interfere with the binding of CD40L to CD40. The present sequence is  
XX CC human CD40 antigen. CD40 is a 50 kDa type 1 membrane glycoprotein  
XX CC expressed on a variety of cells, including B cells. CD40 is critical for  
XX CC B cell function. The non-antibody molecules of the present invention are  
XX CC useful for treating autoimmune, cell-mediated and antibody-mediated  
XX CC diseases, and conditions in which immunogenic proteins are used  
XX CC therapeutically

XX SQ Sequence 277 AA;

Query Match 86.0%; Score 785; DB 4; Length 277;  
Best Local Similarity 95.1%; Pred. No. 4e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRLPQCVMGCLLTAVHPEPTACREKQYLINSQCCSLCOPGQKLVSDCTEFTETECCL 60  
DB 1 MVRLPQCVMGCLLTAVHPEPTACREKQYLINSQCCSLCOPGQKLVSDCTEFTETECCL 60  
QY 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
DB 61 PCGESEFLDTWNRTHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACSCV 120  
QY 121 LHRSCSPGFGVKQIARPKTWLC 143  
DB 121 LHRSCSPGFGVKQIATGVSDTIC 143  
RESULT 14  
AAB37807  
ID AAB37807 standard; protein; 277 AA.  
XX AC AAB37807;  
XX DT 23-FEB-2001 (first entry)  
XX DE Human CD40.  
XX KW Human; CD40; antiviral; anti-HIV; CD40 stimulant;  
XX KW human immunodeficiency virus; HIV; cancer; organ transplantation.

XX 20-NOV-2003 (first entry)  
XX CD40 splice variant protein #SEQ ID 2.  
XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;  
XX inflammatory disease; cancer; atherosclerosis; acute injury.  
XX Homo sapiens.  
XX WO2003070768-A2.  
XX 28-AUG-2003.  
XX 24-FEB-2003; 2003WO-IB000665.  
XX 22-FEB-2002; 2002US-0358877P.  
XX (COMP-) COMPUGEN LTD.  
XX Bernstein J, Mintz L, Eshel D;  
XX WPI; 2003-697601/66.  
XX N-PSDB; ADA25629.  
XX Protein, useful for preparing a composition for modulating CD40-CD154  
XX interactions in an individual for treating chronic-inflammatory disease,  
XX cancer, atherosclerosis or acute injury.  
XX Claim 1; Page 76-77; 92pp; English.  
XX The invention relates to substantially pure CD40 splice variant proteins  
XX which include tail sequences. Also disclosed is a pharmaceutical  
XX composition comprising the protein and a carrier, an in vitro method of  
XX detecting whether an individual is expressing the protein, and a method  
XX for modulating CD40-CD154 interactions in an individual. The protein of  
XX -the invention is useful for preparing a composition for modulating CD40-  
XX CD154 interactions in an individual for treating chronic inflammatory  
XX disease, cancer, atherosclerosis or acute injury. The current sequence  
XX represents CD40 splice variant protein.  
XX Sequence 244 AA;  
Query Match 86.0%; Score 785; DB 6; Length 244;  
Best Local Similarity 95.1%; Pred. No. 3.6e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCLCPQKLVSDCTFTETEC 60  
Db 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCLCPQKLVSDCTFTETEC 60  
QY 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
Db 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPGFGVKQIATGVSDTIC 143  
Db 121 LHRSCSPGFGVKQIATGVSDTIC 143  
RESULT 11  
AAV33499  
ID AAV33499 standard; protein; 276 AA.  
XX AC AAV33499;  
XX 19-JAN-2000 (first entry)  
XX Human CD40 protein.  
XX Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;  
XX huntingtin polypeptide; Machado-Joseph disease; SCAL; SCA2; SCA6;  
XX atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;

XX Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;  
XX dentatorubralpallidoluysian atrophy; cell proliferation; cell survival;  
XX neoplastic; malignant; autoimmune; fibrotic; CD40.  
XX Homo sapiens.  
XX WO9945944-A1.  
XX 16-SEP-1999.  
XX 11-MAR-1999; 99WO-US005250.  
XX 12-MAR-1998; 98US-00041886.  
XX (BURN-) BURNHAM INST.  
XX Bredezen DE, Rabizadeh S;  
XX WPI; 1999-561617/47.  
XX N-PSDB; AAZ23432.  
XX New proapoptotic dependence peptides, used to develop products for  
XX treating, e.g. Alzheimer's disease.  
XX Disclosure; Page 170-171; 199pp; English.  
XX This invention describes novel pure proapoptotic dependence peptides  
XX which comprise a sequence of an active dependence domain selected from  
XX dependence polypeptides consisting of p75NTR, androgen receptor, DCC,  
XX huntingtin polypeptide, Machado-Joseph disease gene product, SCAL, SCA2,  
XX SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of  
XX inducing cell death and can be used to develop products to mediate or  
XX inhibit apoptosis. The methods can be used for reducing the severity of a  
XX proapoptotic dependence domain mediated pathological conditions e.g.  
XX Huntington's disease, Alzheimer's disease, Kennedy's disease, Machado-  
XX spinocerebellar ataxia, dentatorubralpallidoluysian atrophy, Machado-  
XX Joseph disease, stroke or head trauma. They can also be used for reducing  
XX the severity of a pathological condition mediated by upregulated cell  
XX proliferation or cell survival e.g. neoplastic, malignant, autoimmune or  
XX fibrotic conditions. This sequence represents the human CD40 polypeptide  
XX described in the method of the invention  
XX Sequence 276 AA;  
Query Match 86.0%; Score 785; DB 2; Length 276;  
Best Local Similarity 95.1%; Pred. No. 4e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCLCPQKLVSDCTFTETEC 60  
Db 1 MVRPLQCVLWGCLLTAVHPPTACREKQYLINSQCCLCPQKLVSDCTFTETEC 60  
QY 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
Db 61 PCGSEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPGFGVKQIATGVSDTIC 143  
Db 121 LHRSCSPGFGVKQIATGVSDTIC 143  
RESULT 12  
AAV52701  
ID AAV52701 standard; protein; 277 AA.  
XX AC AAV52701;  
XX 26-JAN-2000 (first entry)  
XX Human CD40 protein.  
XX Identification; genetic target; gene modulation; human;  
XX antisense oligonucleotide; phosphorothioate; target validation;

```

Db      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLQPGGKLVSDCTFTETEC 60
QY      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
Db      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
QY      121  LHRSCSPGFGVKQIAVRPXTWLC 143
Db      121  LHRSCSPGFGVKQIAVGSDTIC 143

RESULT 8
ADA25636
ID      ADA25636 standard; protein; 229 AA.
XX
AC      ADA25636;
XX
DT      20-NOV-2003 (first entry)
XX
DE      CD40 splice variant protein #SEQ ID 8.
XX
KW      CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
KW      inflammatory disease; cancer; atherosclerosis; acute injury.
XX
OS      Homo sapiens.
XX
PN      WO2003070768-A2.
XX
PD      28-AUG-2003.
XX
PF      24-FEB-2003; 2003WO-IB000665.
XX
PR      22-FEB-2002; 2002US-0358877P.
XX
PA      (COMP-) COMPUGEN LTD.
XX
PI      Bernstein J, Mintz L, Eshel D;
XX
DR      WPI; 2003-697601/66.
XX
DR      N-ESDB; ADA25633.
XX
PT      Protein, useful for preparing a composition for modulating CD40-CD154
PT      interactions in an individual for treating chronic inflammatory disease,
PT      cancer, atherosclerosis or acute injury.
XX
PS      Claim 1; Page 84-85; 92pp; English.
XX
CC      The invention relates to substantially pure CD40 splice variant proteins
CC      which include tail sequences. Also disclosed is a pharmaceutical
CC      composition comprising the protein and a carrier, an in vitro method of
CC      detecting whether an individual is expressing the protein, and a method
CC      for modulating CD40-CD154 interactions in an individual. The protein of
CC      the invention is useful for preparing a composition for modulating CD40-
CC      CD154 interactions in an individual for treating chronic inflammatory
CC      disease, cancer, atherosclerosis or acute injury. The current sequence
CC      represents CD40 splice variant protein.
XX
SQ      Sequence 229 AA;

Query Match      86.0%; Score 785; DB 6; Length 229;
Best Local Similarity 95.1%; Pred. No. 3.3e-58;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLQPGGKLVSDCTFTETEC 60
Db      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLQPGGKLVSDCTFTETEC 60
QY      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
Db      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
QY      121  LHRSCSPGFGVKQIAVRPXTWLC 143
Db      121  LHRSCSPGFGVKQIAVGSDTIC 143

RESULT 9
ADA25634
ID      ADA25634 standard; protein; 237 AA.
XX
AC      ADA25634;
XX
DT      20-NOV-2003 (first entry)
XX
DE      CD40 splice variant protein #SEQ ID 6.
XX
KW      CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
KW      inflammatory disease; cancer; atherosclerosis; acute injury.
XX
OS      Homo sapiens.
XX
PN      WO2003070768-A2.
XX
PD      28-AUG-2003.
XX
PF      24-FEB-2003; 2003WO-IB000665.
XX
PR      22-FEB-2002; 2002US-0358877P.
XX
PA      (COMP-) COMPUGEN LTD.
XX
PI      Bernstein J, Mintz L, Eshel D;
XX
DR      WPI; 2003-697601/66.
XX
DR      N-ESDB; ADA25633.
XX
PT      Protein, useful for preparing a composition for modulating CD40-CD154
PT      interactions in an individual for treating chronic inflammatory disease,
PT      cancer, atherosclerosis or acute injury.
XX
PS      Claim 1; Page 82-83; 92pp; English.
XX
CC      The invention relates to substantially pure CD40 splice variant proteins
CC      which include tail sequences. Also disclosed is a pharmaceutical
CC      composition comprising the protein and a carrier, an in vitro method of
CC      detecting whether an individual is expressing the protein, and a method
CC      for modulating CD40-CD154 interactions in an individual. The protein of
CC      the invention is useful for preparing a composition for modulating CD40-
CC      CD154 interactions in an individual for treating chronic inflammatory
CC      disease, cancer, atherosclerosis or acute injury. The current sequence
CC      represents CD40 splice variant protein.
XX
SQ      Sequence 237 AA;

Query Match      86.0%; Score 785; DB 6; Length 237;
Best Local Similarity 95.1%; Pred. No. 3.4e-58;
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLQPGGKLVSDCTFTETEC 60
Db      1  MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLQPGGKLVSDCTFTETEC 60
QY      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
Db      61  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTTCTCEGWHCTSEACESC 120
QY      121  LHRSCSPGFGVKQIAVRPXTWLC 143
Db      121  LHRSCSPGFGVKQIAVGSDTIC 143

RESULT 10
ADA25630
ID      ADA25630 standard; protein; 244 AA.
XX
AC      ADA25630;

```

CC therapy procedures. The current sequence is that of the human CD40 (D1-  
CC D3)-6XHis mutant extracellular domain protein of the invention.

XX  
SQ Sequence 153 AA;

Query Match 86.0%; Score 785; DB 7; Length 153;  
Best Local Similarity 95.1%; Pred. No. 2.2e-58;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLMGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60  
Db 1 MVRPLQCVLMGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACSCV 120  
Db 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACSCV 120

QY 121 LHRSCSPFGVKGQIAVRPKTWLC 143  
Db 121 LHRSCSPFGVKGQIAVGSDTIC 143

## RESULT 6

ADA25632

ID ADA25632 standard; protein; 191 AA.

XX

AC ADA25632;

XX

DT 20-NOV-2003 (first entry)

XX

DE CD40 splice variant protein #SEQ ID 4.

XX

KW CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;  
KW inflammatory disease; cancer; atherosclerosis; acute injury.

XX

OS Homo sapiens.

XX

PN WO2003070768-A2.

XX

PD 28-AUG-2003.

XX

PF 24-FEB-2003; 2003WO-IB000665.

XX

PR 22-FEB-2002; 2002US-0358877P.

XX

PA (COMP-) COMPUGEN LTD.

XX

PI Bernstein J, Mintz L, Eshel D;

XX

DR WPI; 2003-697601/66.

XX

DR N-PSDB; ADA25631.

XX

PT Protein, useful for preparing a composition for modulating CD40-CD154  
PT interactions in an individual for treating chronic inflammatory disease,  
PT cancer, atherosclerosis or acute injury.

XX

PS Claim 1; Page 79-80; 92pp; English.

XX

CC The invention relates to substantially pure CD40 splice variant proteins  
CC which include tail sequences. Also disclosed is a pharmaceutical  
CC composition comprising the protein and a carrier, an in vitro method of  
CC detecting whether an individual is expressing the protein, and a method  
CC for modulating CD40-CD154 interactions in an individual. The protein of  
CC the invention is useful for preparing a composition for modulating CD40-  
CC CD154 interactions in an individual for treating chronic inflammatory  
CC disease, cancer, atherosclerosis or acute injury. The current sequence  
CC represents CD40 splice variant protein.

XX  
SQ Sequence 191 AA;

Query Match

Best Local Similarity 86.0%; Score 785; DB 6; Length 191;

Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLMGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

Db 1 MVRPLQCVLMGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACSCV 120

Db 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEBWHCTSEACSCV 120

QY 121 LHRSCSPFGVKGQIAVRPKTWLC 143

Db 121 LHRSCSPFGVKGQIATGVSDTIC 143

## RESULT 7

ADE28516

ID ADE28516 standard; protein; 197 AA.

XX

AC ADE28516;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human CD40-6XHis wild-type extracellular domain protein.

XX

KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; wild-type; extracellular domain; CD40-6XHis.

XX

OS Synthetic.

OS

OS Homo sapiens.

XX

PN WO2003040170-A2.

XX

PD 15-MAY-2003.

XX

PF 08-NOV-2002; 2002WO-US036107.

XX

PR 09-NOV-2001; 2001US-0348980P.

XX

PA (PFIZ ) PFIZER PROD INC.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX

DR WPI; 2003-441521/41.

XX

PT New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.

XX

PS Example 14; SEQ ID NO 139; 177pp; English.

XX

CC The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human CD40-6XHis  
CC wild-type extracellular domain protein of the invention.

XX

SQ Sequence 197 AA;

XX

Query Match 86.0%; Score 785; DB 7; Length 197;

Best Local Similarity 95.1%; Pred. No. 2.9e-58;

Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLMGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTEFTETEC 60

CC capable of binding to a CD40R variant and affecting the binding affinity  
CC of the variant to a CD40 ligand  
XX  
SQ Sequence 246 AA;  
Query Match 86.3%; Score 787.5; DB 4; Length 246;  
Best Local Similarity 83.0%; Pred. No. 2.2e-58;  
Matches 142; Conservative 5; Mismatches 11; Indels 13; Gaps 2;  
QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL 60  
QY 61 PCGSEFELDTWNRETHCHQHKYCDPNLGLRVQOQKGTSETDTICTCEGWHCTSEACESC 120  
DB 61 PCGSEFELDTWNRETHCHQHKYCDPNLGLRVQOQKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPFGVGKQIAVRPKTW-----LCNRQAQTRLMLSVVPRI 159  
DB 121 LHRSCSPFGVGKQIACTETDLVVQOAGTNKTDVVCQPQDLRALV-VIPII 170  
RESULT 4  
ABR63594  
ID ABR63594 standard; protein; 246 AA.  
XX  
AC ABR63594;  
DT 18-SEP-2003 (first entry)  
XX  
DE Human oxifan protein.  
XX  
KW Metabolic research; oxifan; agonist; antagonist; body mass; obesity;  
KW hyperlipidaemia; atherosclerosis; insulin resistance; diabetes;  
KW hypertension; anorectic; antilipemic; antiarteriosclerotic; antidiabetic;  
KW hypotensive; immunomodulator; anti-HIV; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..20  
FT /label= signal\_peptide  
FT Domain 21..161  
FT /label= EC\_domain  
FT Domain 162..184  
FT /label= transmembrane\_domain  
FT Domain 185..246  
FT /label= IC\_domain  
XX  
FN WO2003049759-A1.  
XX  
PD 19-JUN-2003.  
XX  
PF 14-OCT-2002; 2002WO-IB004634.  
XX  
PR 13-DEC-2001; 2001US-0340414P.  
XX  
XX (GEST ) GENSET SA.  
XX  
XX Dialynas D, Scalia A;  
XX  
XX WPI; 2003-569079/53.  
XX  
XX N-PSDB; ACC85399.  
XX  
XX New agonist or antagonist of Oxifan activity, useful for preventing or  
XX treating metabolic disorders such as obesity or obesity-related disorders  
XX (e.g. hyperlipidaemia) or those associated with excessive weight loss  
XX (e.g. anorexia).  
XX  
XX Disclosure; Page 33-34; 37pp; English.  
XX  
XX The present invention relates to agonists and antagonists of oxifan, a  
XX member of the tumour necrosis factor receptor superfamily. These can be

CC used in preventing and treating obesity-related diseases, including  
CC hyperlipidaemia, atherosclerosis, insulin resistance, diabetes and  
CC hypertension. The present sequence is the human oxifan protein described  
XX in the invention  
SQ Sequence 246 AA;  
Query Match 86.3%; Score 787.5; DB 6; Length 246;  
Best Local Similarity 83.0%; Pred. No. 2.2e-58;  
Matches 142; Conservative 5; Mismatches 11; Indels 13; Gaps 2;  
QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL 60  
QY 61 PCGSEFELDTWNRETHCHQHKYCDPNLGLRVQOQKGTSETDTICTCEGWHCTSEACESC 120  
DB 61 PCGSEFELDTWNRETHCHQHKYCDPNLGLRVQOQKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPFGVGKQIAVRPKTW-----LCNRQAQTRLMLSVVPRI 159  
DB 121 LHRSCSPFGVGKQIACTETDLVVQOAGTNKTDVVCQPQDLRALV-VIPII 170  
RESULT 5  
ADE28517  
ID ADE28517 standard; protein; 153 AA.  
XX  
AC ADE28517;  
DT 29-JAN-2004 (first entry)  
XX  
DE Human CD40 (D1-D3)-6XHis mutant extracellular domain protein.  
XX  
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; mutant; mutein; extracellular domain; (D1-D3)-6XHis.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FN WO2003040170-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-US036107.  
XX  
PR 09-NOV-2001; 2001US-0348980P.  
XX  
XX (PFIZ ) PFIZER PROD INC.  
XX (ABGE-) ABGENIX INC.  
XX  
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX WPI; 2003-441521/41.  
XX  
XX New chimeric or human monoclonal antibody or its antigen-binding portion  
XX that specifically binds to and activates human CD40, useful for enhancing  
XX an immune response in a human, or treating cancer, HIV, neutropenia or  
XX viral infections.  
XX  
XX Example 14; SEQ ID NO 140; 177pp; English.  
XX  
XX The invention relates to a novel chimeric or human monoclonal antibody or  
XX its antigen-binding portion that specifically binds to and activates  
XX human CD40. The anti-CD40 antibody of the invention demonstrates  
XX cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
XX activities and may be useful for treating a hyperproliferative disorder  
XX such as cancer, viral and bacterial infection or genetic, primary or  
XX combined immunodeficiency conditions including neutropenia or HIV  
XX infection. The anti-CD40 antibodies may also be useful for detecting CD40  
XX in a biological sample in vitro or in vivo, as well as during gene



CC e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple  
CC sclerosis, inflammatory diseases and graft versus host disease. Also  
CC claimed are methods for detecting the presence of a variant CD40R in a  
CC sample, for determining the level of variant CD40R in a sample, and for  
CC determining the ratio between the level of a CD40R variant acid and the  
CC level of original CD40R, and a method for identifying candidate compounds  
CC capable of binding to a CD40R variant and affecting the binding affinity  
CC of the variant to a CD40 ligand  
XX

SQ Sequence 160 AA;

Query Match 100.0%; Score 913; DB 4; Length 160;  
Best Local Similarity 100.0%; Pred. No. 4e-69;  
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETEC 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETEC 60  
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPGFGVKQIAVRPKTWCNRAQTRLMLSVVPRIG 160  
DB 121 LHRSCSPGFGVKQIAVRPKTWCNRAQTRLMLSVVPRIG 160

RESULT 2

ADA25635  
ID ADA25635 standard; protein; 156 AA.

XX ADA25635;

XX 20-NOV-2003 (first entry)

XX CD40 splice variant protein #SEQ ID 7.

XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;  
XX inflammatory disease; cancer; atherosclerosis; acute injury.

XX Homo sapiens.

XX WO2003070768-A2.

XX 28-AUG-2003.

XX 24-FEB-2003; 2003WO-IB000665.

XX 22-FEB-2002; 2002US-0358877P.

XX (COMP-) COMPUGEN LTD.

XX Bernstein J, Mintz L, Eshel D;

XX WPI; 2003-697601/66.

XX Protein, useful for preparing a composition for modulating CD40-CD154  
XX interactions in an individual for treating chronic inflammatory disease,  
XX cancer, atherosclerosis or acute injury.

XX Claim 1; Page 83-84; 92pp; English.

XX The invention relates to substantially pure CD40 splice variant proteins  
XX which include tail sequences. Also disclosed is a pharmaceutical  
XX composition comprising the protein and a carrier, an in vitro method of  
XX detecting whether an individual is expressing the protein, and a method  
XX for modulating CD40-CD154 interactions in an individual. The protein of  
XX the invention is useful for preparing a composition for modulating CD40-  
XX CD154 interactions in an individual for treating chronic inflammatory  
XX disease, cancer, atherosclerosis or acute injury. The current sequence  
XX represents CD40 splice variant protein.

SQ Sequence 156 AA;

Query Match 97.6%; Score 891; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.8e-67;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETEC 60  
DB 1 MVRPLQCVLWGCLLTAVHPEPTACREKQYLINSQCSCLCQPGQKLVSDCTFTETEC 60  
QY 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
DB 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGTSETDTICTCEGWHCTSEACESC 120  
QY 121 LHRSCSPGFGVKQIAVRPKTWCNRAQTRLMLSVV 156  
DB 121 LHRSCSPGFGVKQIAVRPKTWCNRAQTRLMLSVV 156

RESULT 3

AAB20170  
ID AAB20170 standard; protein; 246 AA.

XX AAB20170;

XX 30-APR-2001 (first entry)

XX Human CD40 receptor splice variant.

XX CD40 receptor; CD40R; human; splice variant; antiinflammatory;  
XX immunosuppressive; antiarthritic; antirheumatic; dermatological;  
XX neuroprotective; therapy; diagnosis.

XX Homo sapiens.

XX WO200105967-A1.

XX 25-JAN-2001.

XX 19-JUL-2000; 2000WO-IL000427.

XX 20-JUL-1999; 99IL-00130989.

XX (COMP-) COMPUGEN LTD.

XX Savitzky K, Khosravi R, Elazar M;

XX WPI; 2001-147341/15.

XX N-PSDB; AAF30276.

XX Nucleic acid encoding alternative splicing variant of CD40 receptor,  
XX useful for treating inflammatory diseases, autoimmune diseases, and graft  
XX versus host reaction.

XX Claim 4; Page 62-63; 70pp; English.

XX The present sequence is that of a novel splice variant of the human CD40  
XX receptor (CD40R). The variant has the extracellular domain of the native  
XX protein from the signal peptide up to the amino acid before the  
XX transmembrane region. 6 Novel splice variants (see AAB20169-74) of human  
XX and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
XX expression vectors, host cells and antibodies are claimed. Also claimed  
XX is a pharmaceutical composition consisting of a variant CD40R polypeptide  
XX for treatment of diseases which can be ameliorated, cured or prevented by  
XX either decreasing the level or of at least 1 ligand of CD40R, or by  
XX increasing the level of a CD40R variant; antibodies can be used to reduce  
XX the level of a CD40R variants. The diseases include autoimmune diseases  
XX e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple  
XX sclerosis, inflammatory diseases and graft versus host disease. Also  
XX claimed are methods for detecting the presence of a variant CD40R in a  
XX sample, for determining the level of variant CD40R in a sample, and for  
XX determining the ratio between the level of a CD40R variant acid and the  
XX level of original CD40R, and a method for identifying candidate compounds

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OM protein - protein search, using sw model

Run on: July 21, 2004, 09:59:29 ; Search time 54 Seconds  
(without alignments)  
837.178 Million cell updates/sec

Title: US-10-031-607-7

Perfect score: 913

Sequence: 1 MVRPLPQCVLWGCLLFAVHP.....WLCNRQAQTRMLSVVPRIG 160

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*

1: Geneseqp1990s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	913	100.0	160	4	AAB20169 Human CD4
2	891	97.6	156	6	ADA25635 CD40 spli
3	787.5	86.3	246	4	AAB20170 Human CD4
4	787.5	86.3	246	6	ABR63594 Human CD4
5	785	86.0	153	7	ADA28517 Human CD4
6	785	86.0	191	6	ADA25632 CD40 spli
7	785	86.0	197	7	ADA28516 Human CD4
8	785	86.0	229	6	ADA25636 CD40 spli
9	785	86.0	237	6	ADA25634 CD40 spli
10	785	86.0	244	6	ADA25630 CD40 spli
11	785	86.0	276	2	AAY33499 Human CD4
12	785	86.0	277	2	AAY52701 Human CD4
13	785	86.0	277	4	AAB4892 Human CD4
14	785	86.0	277	4	AAB37807 Human CD4
15	785	86.0	277	4	AAB50520 Human CD4
16	785	86.0	277	5	AAB30354 Human CD4
17	785	86.0	277	5	AAQ18051 CD40 B-ce
18	785	86.0	277	6	ABR58624 Human can
19	785	86.0	277	6	ABR40010 Human Mox
20	785	86.0	277	6	ABG73061 Human CD4
21	785	86.0	277	6	ADA25652 CD40 wild
22	785	86.0	277	7	ADD18920 Human dis
23	780	85.4	281	5	ABP70127 Human NOV
24	779	85.3	225	5	ABP70126 Human NOV
25	778	85.2	237	6	ADA09880 Human rec

26	778	85.2	277	7	ADE25748 Human pro
27	763	83.6	277	2	AAR38859 CD40 prot
28	760	83.2	277	2	AAY32191 CD40 prot
29	759	83.1	306	4	ABG22935 Novel hum
30	664	72.7	125	5	ABP70128 Human NOV
31	648	71.0	163	6	ADA49703 Extracell
32	638	69.9	163	3	AAY94713 Tumour ne
33	619	67.8	278	3	AAY95322 Pig costi
34	611	66.9	111	7	ADE28518 Human CD4
35	568	62.2	274	3	AAY58212 Canine CD
36	548	60.0	160	6	ADA25638 Murine CD
37	532	58.3	839	4	ABG22934 Novel hum
38	526	57.6	156	4	AAB20171 Mouse CD4
39	500	54.8	255	3	AAY58213 Canine ma
40	483	52.9	195	4	AAB20173 Mouse CD4
41	483	52.9	197	4	AAB66982 CD40 prot
42	483	52.9	203	4	AAB20172 Mouse CD4
43	483	52.9	281	3	AAY94715 Murine CD
44	465	50.9	211	4	AAB20174 Mouse CD4
45	447	49.0	75	2	AAW94647 TNF-R ext

## ALIGNMENTS

RESULT 1  
AAB20169  
ID AAB20169 standard; protein; 160 AA.

XX AC AAB20169;

XX DT 30-APR-2001 (first entry)

XX DE Human CD40 receptor splice variant.

XX KW CD40 receptor; CD40R; human; splice variant; antiinflammatory;  
XX KW immunosuppressive; antiarthritic; antirheumatic; dermatological;  
XX KW neuroprotective; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WC200105967-A1.

XX PD 25-JAN-2001.

XX PF 19-JUL-2000; 2000MO-IL000427.

XX PR 20-JUL-1999; 99IL-00130989.

XX (COMP-) COMPUGEN LTD.

XX PI Savitzky K, Khosravi R, Elazar M;

XX DR WPI; 2001-147341/15.

XX DR N-PSDB; AAF30275.

XX PT Nucleic acid encoding alternative splicing variant of CD40 receptor,  
XX PT useful for treating inflammatory diseases, autoimmune diseases, and graft  
XX PT versus host reaction.

XX PS Claim 4; Page 61; 70pp; English.

XX CC The present sequence is that of a novel splice variant of the human CD40  
XX CC receptor (CD40R). The variant has the extracellular domain of the native  
XX CC protein from the signal peptide up to the amino acid before the  
XX CC transmembrane region. 6 Novel splice variants (see AAB20169-74) of human  
XX CC and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
XX CC expression vectors, host cells and antibodies are claimed. Also claimed  
XX CC is a pharmaceutical composition consisting of a variant CD40R polypeptide  
XX CC for treatment of diseases which can be ameliorated, cured or prevented by  
XX CC either decreasing the level or of at least 1 ligand of CD40R, or by  
XX CC increasing the level of a CD40R variant; antibodies can be used to reduce  
XX CC the level of a CD40R variants. The diseases include autoimmune diseases

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	809	100.0	809	4	AAf30280	AAf30280 Mouse CD4
2	742	91.7	776	4	AAf30278	AAf30278 Mouse CD4
3	679	83.9	1579	6	ABQ74499	ABQ74499 Mouse CD4
4	547	67.6	788	4	AAf30279	AAf30279 Mouse CD4
5	429.2	53.1	934	4	AAf30277	AAf30277 Mouse CD4
6	312.8	38.7	469	6	ABQ74500	ABQ74500 Mouse CD4
7	280.4	34.7	910	8	ADA25651	ADA25651 CD40 wild
8	280.4	34.7	1004	1	AAf90617	AAf90617 CD40 cDNA
9	280.4	34.7	1004	2	AAf14706	AAf14706 Human CD4
10	280.4	34.7	1004	2	AAfV63454	AAfV63454 Human CD4
11	280.4	34.7	1004	2	AAZ40936	AAZ40936 Human CD4
12	280.4	34.7	1004	2	AAV81198	AAV81198 Human CD4
13	280.4	34.7	1004	2	AAZ23432	AAZ23432 Human CD4
14	280.4	34.7	1004	3	AAf50590	AAf50590 Human cel
15	280.4	34.7	1004	3	AAZ47769	AAZ47769 Human CD4
16	280.4	34.7	1004	4	AAf303184	AAf303184 Human Lym
17	280.4	34.7	1004	6	AAf147328	AAf147328 CD40 B-ce
18	280.4	34.7	1004	7	ACf56689	ACf56689 Human sig
19	280.4	34.7	1004	7	ACC72771	ACC72771 Human can
20	280.4	34.7	1004	7	ACC00289	ACC00289 Human Mox
21	280.4	34.7	1004	7	ABx14593	ABx14593 Human CD4
22	280.4	34.7	1004	9	ADd18921	ADd18921 Human dis
23	280.4	34.7	1004	9	ADf85051	ADf85051 Farnesyl

CC amino acids. In addition, there is a 9-amino acid insert at position 86  
CC of the original protein, instead of the original Asn. The variant is  
CC missing part of TNFR Cys repeat 4, the transmembrane domain and the  
CC cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of human  
CC and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
CC expression vectors, host cells and anti-CD40R antibodies are claimed.  
CC Also claimed is a pharmaceutical composition consisting of an expression  
CC vector comprising a CD40R nucleic acid, for treatment of diseases which  
CC can be ameliorated, cured or prevented by either decreasing the level or  
CC of at least 1 ligand of CD40R, by increasing the level of a CD40R  
CC variant, or by reducing the level of a CD40R variant. The diseases  
CC include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus  
CC erythematosus, and multiple sclerosis, inflammatory diseases and graft  
CC versus host disease. Also claimed are methods for detecting the presence  
CC of a variant nucleic acid sequence of CD40R in a sample, for determining  
CC the level of variant nucleic acid sequences of CD40R in a sample, and for  
CC determining the ratio between the level of a CD40R variant nucleic acid  
CC and the level of the original CD40R, e.g. using a nucleic acid chip  
XX  
SQ Sequence 809 BP; 194 A; 213 C; 229 G; 173 T; 0 U; 0 Other;  
Query Match 100.0%; Score 809; DB 4; Length 809;  
Best Local Similarity 100.0%; Pred. No. 4e-249;  
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCTGTCTTTCCTCGCTGTGCGCGCTATGCGGCTGCTGTGTGACAGCGGTCCATCTA 60  
DB 1 ATGCTGTCTTTCCTCGCTGTGCGCGCTATGCGGCTGCTGTGTGACAGCGGTCCATCTA 60  
QY 61 GGGCAGTGTGTACGTGCTGAGTGAACAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
DB 61 GGGCAGTGTGTACGTGCTGAGTGAACAACAGTACCTCCACGATGCCAGTCTGTGATTG 120  
QY 121 TGCAGCCAGGAAGCGACTGACGAAGCCACTGACAGCTCTTGAGAGAGACCCCAATGCCAC 180  
DB 121 TGCAGCCAGGAAGCGACTGACGAAGCCACTGACAGCTCTTGAGAGAGACCCCAATGCCAC 180  
QY 181 CCATGTGACTCAGCGCAATTCAGCCCGAGTGAACAGGAGATTCGCTGTCCACGAGCAC 240  
DB 181 CCATGTGACTCAGCGCAATTCAGCCCGAGTGAACAGGAGATTCGCTGTCCACGAGCAC 240  
QY 241 AGACACTGTGAACCCAGTGGGTGGGTGCTGGGAAGGGATCAAGGGCTTCGGGTAAAG 300  
DB 241 AGACACTGTGAACCCAGTGGGTGGGTGCTGGGAAGGGATCAAGGGCTTCGGGTAAAG 300  
QY 301 AAGGAGGCGCACCGAGATCAGACACTGTCTGTACCTGTAGGAGAGACAACTGCACC 360  
DB 301 AAGGAGGCGCACCGAGATCAGACACTGTCTGTACCTGTAGGAGAGACAACTGCACC 360  
QY 361 AGCAAGGATTGCGAGGATGTGCTCAGCACACGCGCTGTATCCCTGGCTTTGGAGTTATG 420  
DB 361 AGCAAGGATTGCGAGGATGTGCTCAGCACACGCGCTGTATCCCTGGCTTTGGAGTTATG 420  
QY 421 GAGATGCGCACTGAGACACTGATACCGTCTGTATCCCTGCCAGTCGCTTCTCTCC 480  
DB 421 GAGATGCGCACTGAGACACTGATACCGTCTGTATCCCTGCCAGTCGCTTCTCTCC 480  
QY 481 AATCAGTCACTACATTTTCGAAAAGTGTATCCCTGGACAGAGTTTAAAGTCCCGGATGCG 540  
DB 481 AATCAGTCACTACATTTTCGAAAAGTGTATCCCTGGACAGAGTTTAAAGTCCCGGATGCG 540  
QY 541 AGCCCTGCTGTGATCTGCTGTGATGGGATCCTCATCACCATTTCGGGGTGTTCCT 600  
DB 541 AGCCCTGCTGTGATCTGCTGTGATGGGATCCTCATCACCATTTCGGGGTGTTCCT 600  
QY 601 CTATATCAAAAAGTGTCAAGAAACCAAGGATTAAGATGATTTACCCCTCGCGCTCG 660  
DB 601 CTATATCAAAAAGTGTCAAGAAACCAAGGATTAAGATGATTTACCCCTCGCGCTCG 660  
QY 661 ACGGCAAGATCCCGAGAGATGGAAGATTATCCGGTCAATACACCGCTCTCCAGTGA 720  
DB 661 ACGGCAAGATCCCGAGAGATGGAAGATTATCCGGTCAATACACCGCTCTCCAGTGA 720

QY 721 GGAGACACTGCACCGGTGTGACGCTGTCCACACAGAGGATCGTAAAGAGATCGCATCTC 780  
DB 721 GGAGACACTGCACCGGTGTGACGCTGTCCACACAGAGGATCGTAAAGAGATCGCATCTC 780  
QY 781 AGTCGAGGAGCGGCGAGGTGACAGACAGCA 809  
DB 781 AGTCGAGGAGCGGCGAGGTGACAGACAGCA 809  
RESULT 2  
AAE30278  
ID AAF30278 standard; cDNA; 776 BP.  
XX  
AC AAF30278;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Mouse CD40 receptor splice variant cDNA clone Mcd40Alt8.  
XX  
XX CD40 receptor; CD40R; mouse; splice variant; antiinflammatory;  
XX immunosuppressive; antirheumatic; antirheumatic; dermatological;  
XX neuroprotective; gene therapy; diagnosis; ss.  
XX  
XX Mus musculus.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..612  
XX FT /\*tag= a  
XX  
XX WC200105967-AL.  
XX  
XX 25-JAN-2001.  
XX  
XX 19-JUL-2000; 2000WO-IL000427.  
XX  
XX 20-JUL-1999; 99IL-00130989.  
XX  
XX (COMP-) COMPUGEN LTD.  
XX  
XX Savitzky K, Khosravi R, Elazar M;  
XX  
XX WPI; 2001-147341/15.  
XX P-PSDB; AAB20172.  
XX  
XX Nucleic acid encoding alternative splicing variant of CD40 receptor,  
XX useful for treating inflammatory diseases, autoimmune diseases, and graft  
XX versus host reaction.  
XX  
XX Claim 1; Page 59-60; 70pp; English.  
XX  
XX The present sequence is that of mouse cDNA encoding splice variant  
XX Mcd40Alt8 (see AAB20172) of the mouse CD40 receptor (CD40R). The variant  
XX contains 165 N-terminal amino acids of the original CD40R sequence  
XX including tumour necrosis factor receptor (TNFR) Cys repeats 1, 2 and 3,  
XX and part of TNFR Cys repeat 4, with 38 alternative C-terminal amino  
XX acids. It is missing part of TNFR repeat 4, the transmembrane domain and  
XX the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of  
XX human and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
XX expression vectors, host cells and anti-CD40R antibodies are claimed.  
XX Also claimed is a pharmaceutical composition consisting of an expression  
XX vector comprising a CD40R nucleic acid, for treatment of diseases which  
XX can be ameliorated, cured or prevented by either decreasing the level or  
XX of at least 1 ligand of CD40R, by increasing the level of a CD40R  
XX variant, or by reducing the level of a CD40R variant. The diseases  
XX include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus  
XX erythematosus, and multiple sclerosis, inflammatory diseases and graft  
XX versus host disease. Also claimed are methods for detecting the presence  
XX of a variant nucleic acid sequence of CD40R in a sample, for determining  
XX the level of variant nucleic acid sequences of CD40R in a sample, and for  
XX determining the ratio between the level of a CD40R variant nucleic acid  
XX and the level of the original CD40R, e.g. using a nucleic acid chip  
XX  
XX Sequence 776 BP; 188 A; 205 C; 213 G; 169 T; 0 U; 0 Other;

Query Match 91.7%; Score 742; DB 4; Length 776;  
 Best Local Similarity 97.0%; Pred. No. 1.4e-227;  
 Matches 776; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

QY 1 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTGCACAGCGTCCATCTA 60  
 Db 1 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTGCACAGCGTCCATCTA 60

QY 61 GGGCAGTGTGTACGTGCAAGTACAAAGTACCTCCAGATGGCAGTGTGTGATTG 120  
 Db 61 GGGCAGTGTGTACGTGCAAGTACAAAGTACCTCCAGATGGCAGTGTGTGATTG 120

QY 121 TGCCAGCAGGAGCGGCTGACAGCCACTGCACAGCTTTGAGAAGACCAATGCCAC 180  
 Db 121 TGCCAGCAGGAGCGGCTGACAGCCACTGCACAGCTTTGAGAAGACCAATGCCAC 180

QY 181 CCATGTGACTCAGGCGAATTTCTCAGCCCACTGAGGAGATTCGCTGTCCACAGCAC 240  
 Db 181 CCATGTGACTCAGGCGAATTTCTCAGCCCACTGAGGAGATTCGCTGTCCACAGCAC 240

QY 241 AGACACTGTGACCCAGTGTGCGGCTGCGGAGGATCAAGGGCTTCGGGTTAAG 300  
 Db 241 AGACACTGTGACCCAGTGTGCGGCTGCGGAGGATCAAGGGCTTCGGGTTAAG 300

QY 301 AAGGAGGCGACCGCAGAAATCAGACACTGTCTGTACTGTGTAAGGAAGCAACACTGCACC 360  
 Db 301 AAGGAGGCGACCGCAGAAATCAGACACTGTCTGTACTGTGTAAGGAAGCAACACTGCACC 360

QY 361 AGCAAGGATTGCGAGGATGTCTCAGCACAGCCCTGTATCCCTGGCTTTGGATTATG 420  
 Db 361 AGCAAGGATTGCGAGGATGTCTCAGCACAGCCCTGTATCCCTGGCTTTGGATTATG 420

QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTATCCCTGCCAGTGGCTTCTTCC 480  
 Db 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTATCCCTGCCAGTGGCTTCTTCC 480

QY 481 AATCAGTCACTCTTTGAAAAGTGTATCCCTGGCAAGGTTTAAAGTCCCGGATCG 540  
 Db 481 AATCAGTCACTCTTTGAAAAGTGTATCCCTGGCAAGGTTTAAAGTCCCGGATCG 540

QY 541 AGCCCTGCTGTCTCTCTGTGATGGGATCTCATCACCATTTTCGGGCTGTCTT 600  
 Db 541 AGCCCTGCTGTCTCTCTGTGATGGGATCTCATCACCATTTTCGGGCTGTCTT 600

QY 601 CTATATCAAAAAGTGGTCAAGAAACCAAGGATATGAGATGTATACCCCTCGCGCTCG 660  
 Db 601 CTATATCAAAAAGTGGTCAAGAAACCAAGGATATGAGATGTATACCCCTCGCGCTCG 660

QY 661 ACGGCAAGATCCCGAGGATGGAAGATTTATCCCGTCAATACACCGTGTCCAGTGA 720  
 Db 661 ACGGCAAGATCCCGAGGATGGAAGATTTATCCCGTCAATACACCGTGTCCAGTGA 720

QY 721 GGAGACACTGCACGGTGTGACGCTGTACACAGGAGGATGTAAAGAGGTTCGATCTC 780  
 Db 721 GGAGACACTGCACGGTGTGACGCTGTACACAGGAGGATGTAAAGAGGTTCGATCTC 780

QY 781 ACTGACGAGCGCGAGGTGA 800  
 Db 781 ACTGACGAGCGCGAGGTGA 800

QY 757 AGTGACGAGCGCGAGGTGA 776  
 Db 757 AGTGACGAGCGCGAGGTGA 776

## RESULT 3

ABQ74499  
 ID ABQ74499 standard; cDNA; 1579 BP.  
 XX  
 AC ABQ74499;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Mouse CD40 nucleotide sequence SEQ ID NO:17.  
 XX  
 KW Mouse; DNA array sequence selection; gene; cDNA microarray; probe;

immunology; tumour; cancer; cancer biology; immune cell; aging;  
 drug testing; infection; autoimmune disease; arthritis; allergy; vaccine;  
 ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200261135-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050618.  
 XX  
 PR 19-DEC-2000; 2000US-00741238.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Lorenz M;  
 XX  
 DR WPI; 2002-608530/65.  
 XX  
 PT New composition comprising an array of cDNA probes immobilized on a solid  
 PT support, useful for diagnostic and screening procedures involving  
 PT immunologically-based sample materials, drug testing or monitoring  
 PT disease progression.  
 XX

Claim 1; Fig 3; 420pp; English.

The present invention describes a composition comprising an array of cDNA probes that are immobilised on a solid support, where the array comprises at least 10-20 probes having sequences selected from the 29 sequences of 192-4655 base pairs given in ABQ74483 to ABQ74511. Also described is a method for selecting DNA sequences for a non-redundant microarray, comprising: (a) providing sequence databases; (b) screening the databases for DNA sequences specific for a species and a tissue found in the species to generate a redundant sequence list; (c) removing redundant sequences from the list to generate a non-redundant cluster list; (d) categorising selected sequences from non-redundant cluster list into at least one module list; and (e) selecting the best representative clones based on the characteristics used to establish the parameters of the module list. The composition comprising the microarrays is useful in diagnostic and screening procedures involving immunologically-based sample materials. It is used in experiments and screens in innate and adaptive basic immunology, tumour immunology, cancer biology of immune cells, aging, drug testing, infection immunology, autoimmune diseases, arthritis, allergy, and vaccine development against these diseases. The composition and method may be used in monitoring the progression of a particular disease, in screening drug treatments for diseases, and in the construction of non-redundant DNA microarrays for different species

Sequence 1579 BP; 391 A; 379 C; 428 G; 381 T; 0 U; 0 Other;

Query Match 83.9%; Score 679; DB 6; Length 1579;  
 Best Local Similarity 90.1%; Pred. No. 3.5e-207;  
 Matches 785; Conservative 0; Mismatches 0; Indels 86; Gaps 2;

QY 1 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTGTGACAGCGTCCATCTA 60  
 Db 9 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTGTGACAGCGTCCATCTA 68

QY 61 GGGCAGTGTGTACGTGCAAGTACAAACAGTACTCCACGATGGCCAGTCTGTGATTG 120  
 Db 69 GGGCAGTGTGTACGTGCAAGTACAAACAGTACTCCACGATGGCCAGTCTGTGATTG 128

QY 121 TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCTCTTGAGAAGACCCCAATGCCAC 180  
 Db 129 TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCTCTTGAGAAGACCCCAATGCCAC 188

QY 181 CCATGTGACTCAGGCGAATTTCTCAGCCCACTGAGGAGGATTCGCTGTCCACGAC 240  
 Db 189 CCATGTGACTCAGGCGAATTTCTCAGCCCACTGAGGAGGATTCGCTGTCCACGAC 248

QY 241 AGACACTGTGAACCCAGTGTGGGCTGCTCGGGAAGGATCAAGGGCTTCGGGTTAAG 300  
 Db 241 AGACACTGTGAACCCAGTGTGGGCTGCTCGGGAAGGATCAAGGGCTTCGGGTTAAG 300



Db 457 AATCAGTCATCACTTTTCGAAAAGTGTATCCCTGGACAAGGTTTAAAGTCCCGGATCG 516  
 QY 541 AGCCCTGCTGTCATCTCTGTCGATCGGATCCCTCATCACTTTTCGGGGTGTCTTCT 600  
 Db 517 AGCCCTGCTGTCATCTCTGTCGATCGGATCCCTCATCACTTTTCGGGGTGTCTTCT 576  
 QY 601 CTATATCAAAAAG 613  
 Db 577 CTATATCAGTGAG 589

## RESULT 5

AAAF30277  
 ID AAF30277 standard; cDNA; 934 BP.

XX AAF30277;  
 XX  
 XX 30-APR-2001 (first entry)  
 XX  
 XX Mouse CD40 receptor splice variant cDNA clone Mcd40-pPB1-1-5.  
 XX  
 XX CD40 receptor; CD40R; mouse; splice variant; antiinflammatory;  
 KW immunosuppressive; antiarthritis; antirheumatic; dermatological;  
 KW neuroprotective; gene therapy; diagnosis; ss.  
 XX  
 XX Mus musculus.

XX Key Location/Qualifiers  
 FH CDS 33..503  
 FT /\*tag= a  
 FT

XX WO200105967-A1.

XX 25-JAN-2001.

XX 19-JUL-2000; 2000WO-IL000427.

XX 20-JUL-1999; 99IL-00130989.

XX (COMP-) COMPUGEN LTD.

XX Savitzky K, Khosravi R, Elazar M;

XX WPI; 2001-147341/15.

XX P-PSDB; AAB20171.

XX Nucleic acid encoding alternative splicing variant of CD40 receptor,  
 PT useful for treating inflammatory diseases, autoimmune diseases, and graft  
 PT versus host reaction.

XX Claim 1; Page 59; 70pp; English.

XX The present sequence is that of mouse cDNA encoding splice variant Mcd40-  
 CC pPB1-1-5 (see AAB20171) of the mouse CD40 receptor (CD40R). The variant  
 CC contains 135 N-terminal amino acids of the original sequence including  
 CC tumour necrosis factor receptor (TNFR). Cys repeats 1 and 2, and part of  
 CC TNFR Cys repeat 3, with 21 alternative C-terminal amino acids. It is  
 CC missing the TNFR repeat 4, part of repeat 3, the transmembrane domain and  
 CC the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of  
 CC human and murine CD40R, nucleic acids (see AAF30275-80) encoding them,  
 CC expression vectors, host cells and antibodies are claimed. Also claimed  
 CC is a pharmaceutical composition consisting of an expression vector  
 CC comprising a CD40R nucleic acid, for treatment of diseases which can be  
 CC ameliorated, cured or prevented by either decreasing the level or of at  
 CC least 1 ligand of CD40R, by increasing the level of a CD40R variant, or  
 CC by reducing the level of a CD40R variant. The diseases include autoimmune  
 CC diseases e.g. rheumatoid arthritis, systemic lupus erythematosus, and  
 CC multiple sclerosis, inflammatory diseases and graft versus host disease.  
 CC Also claimed are methods for detecting the presence of a variant nucleic  
 CC acid sequence of CD40R in a sample, for determining the level of variant  
 CC nucleic acid sequences of CD40R in a sample, and for determining the  
 CC ratio between the level of a CD40R variant nucleic acid and the level of  
 CC the original CD40R, e.g. using a nucleic acid chip

XX SQ Sequence 934 BP; 246 A; 218 C; 231 G; 226 T; 0 U; 13 Other;  
 Query Match 53.1%; Score 429.2; DB 4; Length 934;  
 Best Local Similarity 84.5%; Pred. No. 5.Se-127;  
 Matches 541; Conservative 0; Mismatches 43; Indels 56; Gaps 3;  
 QY 1 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTGTGTGACAGGGTCCCATCTA 60  
 Db 33 ATGGTGTCTTTGCTCGGCTGTGCGGCTATGGGCTGCTTGTGTGACAGGGTCCCATCTA 92  
 QY 61 GGGCAGTGTGTTACGTGCACTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTTG 120  
 Db 93 GGGCAGTGTGTTACGTGCACTGACAAACAGTACCTCCACGATGCCAGTCTGTGATTTG 152  
 QY 121 TGGCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTCTTGAGAGAGCCCAATGCCAC 180  
 Db 153 TGGCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTCTTGAGAGAGCCCAATGCCAC 212  
 QY 181 CCATGTGACTCAGGCGGAATTTCTCAGCCCACTGAGGAGAGATTCGCTGTCAACAGCAC 240  
 Db 213 CCATGTGACTCAGGCGGAATTTCTCAGCCCACTGAGGAGAGATTCGCTGTCAACAGCAC 272  
 QY 241 AGACACTGTGAACCCAGTGTGCTGGGGCTGCTGGGAGAGGATCAAGGGCTTCGGGTTAAG 300  
 Db 273 AGACACTGTGAACCCA-----ATCAGGGCTTCGGGTTAAG 308  
 QY 301 AAGGAGGGCACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGGAAGACAACTGCACC 360  
 Db 309 AAGGAGGGCACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGGAAGACAACTGCACC 368  
 QY 361 AGCAAGGATTGCGAGGATGTGTCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG 420  
 Db 369 AGCAAGGATTGCGAGGATGTGTCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG 428  
 QY 421 GAGATGCCACTGAGACCACTGATACCGTCTGTCTCCCTGCCAGTCGGCTTCTTCTCC 480  
 Db 429 GAGATGCCCTGTGAGGATA-----GACTTGAGGTCCTAC 464  
 QY 481 AATCAGTCACTACCTTTTCGAAAAGTGTATCCCTGGACAAGGTTTAAAGTCCCGGATGCG 540  
 Db 465 AGAAAGGAACGAGTCAGACTAATGTCTATCT-----GTGGTTTAAAGTCCCGGATGCG 516  
 QY 541 AGCCCTGCTGTCATCTCTGTCGATGGGCATCTTCATCACCATTTCGGGGTGTCTTCT 600  
 Db 517 AGCCCTGCTGTCATCTCTGTCGATGGGCATCTTCATCACCATTTCGGGGTGTCTTCT 576  
 QY 601 CTATATCAAAAAGTGTGTCAGAAACCAAGGATAATGAG 640  
 Db 577 CTATATCAAAAAGTGTGTCAGAAACCAAGGATCTCGAG 616

## RESULT 6

ABQ74500  
 ID ABQ74500 standard; cDNA; 469 BP.

XX AC ABQ74500;

XX DT 21-OCT-2002 (first entry)

XX Mouse CD40 image clone nucleotide sequence SEQ ID NO:18.

XX Mouse; DNA array sequence selection; gene; cDNA microarray; probe;  
 KW immunology; tumour; cancer; cancer biology; immune cell; aging;  
 KW drug testing; infection; autoimmune disease; arthritis; allergy; vaccine;  
 KW ss.

XX Mus musculus.

XX WO200261135-A2.

XX 08-AUG-2002.

XX PD

XX



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PF 19-DEC-2001; 2001WO-US050618.
XX
XX
XX 19-DEC-2000; 2000US-00741238.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Lorenz M;
XX
XX WPI; 2002-608530/65.
XX
XX New composition comprising an array of cDNA probes immobilized on a solid
XX support, useful for diagnostic and screening procedures involving
XX immunologically-based sample materials, drug testing or monitoring
XX disease progression.
XX
XX Claim 1; Fig 3; 420pp; English.
XX
XX The present invention describes a composition comprising an array of cDNA
XX probes that are immobilised on a solid support, where the array comprises
XX at least 10-20 probes having sequences selected from the 29 sequences of
XX 192-4655 base pairs given in AB074493 to AB074511. Also described is a
XX method for selecting DNA sequences for a non-redundant microarray,
XX comprising: (a) providing sequence databases; (b) screening the databases
XX for DNA sequences specific for a species and a tissue found in the
XX species to generate a redundant sequence list; (c) removing redundant
XX sequences from the list to generate a non-redundant cluster list; (d)
XX categorising selected sequences from non-redundant cluster list into at
XX least one module list; and (e) selecting the best representative clones
XX based on the characteristics used to establish the parameters of the
XX module list. The composition comprising the microarrays is useful in
XX diagnostic and screening procedures involving immunologically-based
XX sample materials. It is used in experiments and screens in innate and
XX adaptive basic immunology, tumour immunology, cancer biology of immune
XX cells, aging, drug testing, infection immunology, autoimmune diseases,
XX arthritis, allergy, and vaccine development against these diseases. The
XX composition and method may be used in monitoring the progression of a
XX particular disease, in screening drug treatments for diseases, and in the
XX construction of non-redundant DNA microarrays for different species
XX
XX
XX Sequence 469 BP; 110 A; 120 C; 136 G; 103 T; 0 U; 0 Other;
XX
XX Query Match 39.7%; Score 312.8; DB 6; Length 469;
XX Best Local Similarity 99.4%; Pred. No. 1e-89;
XX Matches 314; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 494 TTTTCGAAAGTGTATCCCTCGACAGGTTTAAAGTCCCGATGCGAGCCCTGCTGTC 553
XX 1 TTTTCGAAAGTGTATCCCTCGACAGGTTTAAAGTCCCGATGCGAGCCCTGCTGTC 60
XX
XX 554 ATTCTCTGCTGTATGGGCATCCCTCATCACCATTTCCTGGGGTGTTCCTATATCAAAAAG 613
XX 61 ATTCTCTGCTGTATGGGCATCCCTCATCACCATTTCCTGGGGTGTTCCTATATCAAAAAG 120
XX
XX 614 GTGGTCAAGAAACCAAGAGTAATGAGATGTTTACCCCTCGGCTGACGGCAGATCCC 673
XX 121 GTGGTCAAGAAACCAAGAGTAATGAGATGTTTACCCCTCGGCTGACGGCAGATCCC 180
XX
XX 674 CAGGAGATGGAAGATTATCCCGGTCTAATACACCGCTGCTCCAGTGAGGAGACATGTCAC 733
XX 181 CAGGAGATGGAAGATTATCCCGGTCTAATACACCGCTGCTCCAGTGAGGAGACATGTCAC 240
XX
XX 734 GGGTGTGAGCTGTACACAGGAGGATGTTAAAGAGAGTGCATCTCAGTGACAGAGCGG 793
XX 241 GGGTGTGAGCTGTACACAGGAGGATGTTAAAGAGAGTGCATCTCAGTGACAGAGCGG 300
XX
XX 794 CAGGTGACAGACAGCA 809
XX 301 CAGGTGACAGACAGCA 316
XX
XX
XX RESULT 7
XX ADA25651
XX ID ADA25651 standard; DNA; 910 BP.
```

```
XX ADA25651;
XX
XX 20-NOV-2003 (first entry)
XX
XX CD40 wild-type protein encoding DNA #SEQ ID 23.
XX
XX CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
XX inflammatory disease; cancer; atherosclerosis; acute injury; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 48..881
XX FT /*tag= a
XX FT /product= "CD40 wild-type protein"
XX
XX WO2003070768-A2.
XX
XX 28-AUG-2003.
XX
XX 24-FEB-2003; 2003WO-IB000665.
XX
XX 22-FEB-2002; 2002US-0358877P.
XX (COMP-) COMPUGEN LTD.
XX
XX Bernstein J, Mintz L, Eshel D;
XX
XX WPI; 2003-697601/66.
XX
XX P-PSDB; ADA25652.
XX
XX Protein, useful for preparing a composition for modulating CD40-CD154
XX interactions in an individual for treating chronic inflammatory disease,
XX cancer, atherosclerosis or acute injury.
XX
XX Disclosure; Page 90; 92pp; English.
XX
XX The invention relates to substantially pure CD40 splice variant proteins
XX which include tail sequences. Also disclosed is a pharmaceutical
XX composition comprising the protein and a carrier, an in vitro method of
XX detecting whether an individual is expressing the protein, and a method
XX for modulating CD40-CD154 interactions in an individual. The protein of
XX the invention is useful for preparing a composition for modulating CD40-
XX CD154 interactions in an individual for treating chronic inflammatory
XX disease, cancer, atherosclerosis or acute injury. The current sequence
XX represents CD40 wild-type protein encoding DNA.
XX
XX Sequence 910 BP; 212 A; 270 C; 240 G; 188 T; 0 U; 0 Other;
XX
XX Query Match 34.7%; Score 280.4; DB 8; Length 910;
XX Best Local Similarity 62.7%; Pred. No. 3.7e-79;
XX Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;
XX
XX 1 ATGGTGTTCTTTCCTCGGCTGTGCGCGCTATGCGGCTGCTTGTGACAGCGGTCACTCA 60
XX 48 ATGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107
XX
XX 61 GGGCAGTGTGTACGTGTCAGTGACAAACAGTACCTCCACGATGGCCAGTGTGTGATTG 120
XX 108 GAACCCACCTGATGATGAGAGAAACAGTACCTAATAACAGTCACTGCTGTCTTTG 167
XX
XX 121 TGCCAGCAGGAAGCCGACGTGACAAAGCCTGTCACAGCTTTTGAGAGACCAATGCCAC 180
XX 168 TGCCAGCAGCAGACAGAACTGGTGAAGTCACTGTCACAGAGTTCACTGAAACGGAAATGCTT 227
XX
XX 181 CCATGTGACTCAGGCGAATTCCTCAGCCAGTGGAAACAGGAGATTTCCTGTCACACGAC 240
XX 228 CTTGCGGTGAAGCGAATTCCTAGACACCTGGAAACAGAGACACACTGCCACGACAC 287
XX
XX 241 AGACACTGTGAACCCAGTGTGCGGTGCTGGGAGGGATCAAGGGCTTCGGGTTAAG 300
XX 288 AAATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCAG 323
```





Db 801 CAGGAGACTTTACATGGATGCCAACCGTCAACCAGGAGATGCCAAAGAGAGTCGCATC 860  
 QY 779 TCAGTGCAGGAGCGGCAG 796  
 Db 861 TCAGTGCAGGAGAGACAG 878

RESULT 9  
 AAT14706  
 ID AAT14706 standard; cDNA; 1004 BP.  
 XX  
 AC AAT14706;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-OCT-1996 (first entry)  
 XX  
 XX Human CD40 antigen cDNA.  
 DE  
 XX Cell surface antigen; cloning; immunoselection; immunotherapy; therapy;  
 KW diagnosis; vector; CD40; COS; lymphocyte; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US5506126-A.  
 PN  
 XX 09-APR-1996.  
 PD  
 XX 18-OCT-1993; 93US-00139273.  
 PF  
 XX 25-FEB-1988; 88US-00160416.  
 PR 13-JUL-1989; 89US-00379076.  
 PR 13-JUL-1990; 90US-00553759.  
 PR 01-DEC-1992; 92US-00938647.  
 XX  
 PA (GEMO) GEN HOSPITAL CORP.  
 XX  
 XX Seed B, Aruffo A;  
 PI  
 XX WPI; 1996-200279/20.  
 DR  
 XX  
 XX Cloning of cDNA encoding cell surface antigen - useful for isolation of  
 PT diagnostic and therapeutic proteins.  
 FT  
 XX Example 8; Fig 16; 79pp; English.  
 PS  
 XX  
 XX A cDNA clone (AAT14714) codes for human cell surface antigen CD40. It was  
 CC isolated using a rapid immunoselection method in which a cDNA library is  
 CC constructed in mammalian (e.g. COS) cells using novel expression vectors  
 CC (see also AAT14702 and AAT14705), and cells expressing the antigen are  
 CC selected using antibody-coated plates (panning). This immunoselection  
 CC cloning method, developed to clone genes for cell surface antigens of  
 CC human lymphocytes (see also AAT14703-04 and AAT14706-26), has general  
 CC appln. Cell surface antigens are obd. for diagnostic and therapeutic  
 CC use. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;  
 SQ

Query Match 34.7%; Score 280.4; DB 2; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;  
 QY 1 ATGGTGTCTTGGCTCGGCTATGCGCGCTATGGGGCTGCTTGTGTGACAGCGGTCCATCTA 60  
 Db 48 ATGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107  
 QY 61 GGGCAGTGTGTAGTGCAGTGCACACAGTACTCCACGATGCCAGTCTGTGATTTG 120  
 Db 108 GAACACCCACTGTGATGCAGAGAAAACAGTACTTAATAACAGTCACTGCTGCTTTT 167  
 QY 121 TGGCAGCCAGGAGCCGAGTGCACAGCCACTGTCACAGCTCTTGAGAGACCCCAATGCCAC 180  
 Db 168 TGGCAGCCAGGAGCAAACTGGTGTGAGTGTGCTGACAGAGTTCATGAAACGGAATGCC 227

QY 181 CCATGTGACTCAGGCGAATTTCTCAGCCCACTGGGAACAGGGAGATTCTGTCTCACCAGCAC 240  
 Db 228 CTTTGGGTGAAAGCGAATTTCTAGACACCTTGAACAGAGAGACACACTGCGCACGACAC 287  
 QY 241 AGACACTGTGAACCCAGTGCCTGGGGCTGCTGGGAGGGATCAAGGGCTTCGGGTTAAG 300  
 Db 288 AAATACTCGGACCCCA-----ACCTAGGGCTTCGGGTCAG 323  
 QY 301 AAGGAGGCGCACCGCAGAAATCAGACACTGTCTGTACTGTAAAGGAAGGACAACTGCACCC 360  
 Db 324 CAGAGGSCACCTCAGAAACAGACACCATCTGCACCTGTGAAGAAGGCTGSCACTGTACG 383  
 QY 361 AGCAAGGATTGGAGGCAATGTCTCAGCACAGCCCTGTATCCTCGCTTTGGAGTTATG 420  
 Db 384 AGTGAAGGCTGTGAGAGCTGTCTCTGCACCGCTCATGCTCGCCCGCTTTGGGGTCAAG 443  
 QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTCTCATCCTGCCAGTCGGCTTCTTCTCC 480  
 Db 444 CAGATTGCTACAGGGTTTCTGTATACCATCTGCGAGCCCTGCCAGTCGGCTTCTTCTCC 503  
 QY 481 AATCAGTCACTCACTTTTCGAAAAGTGTATCCCTGGACAAGGTTTAA----- 527  
 Db 504 AATGTGTCACTGTCTTTCGAAAATGTCAACCTTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 Db 564 GTTGTGCAACAGGAGGCAAAACAAGACTGATGTTGTCTGTCCTCCAGATCGGCTG 623  
 QY 539 CGAGCCCTGCTGGTCACTCTCTGTGTATGGGCACTCCTCATCACCATTTCGGGGTGT 598  
 Db 624 AGAGCCCTGCTGGTCACTCTCTGTGTATGGGCACTCCTGTTCATCTCTTGGTGTG 683  
 QY 599 CTCATATCAAAAAGTGTCTCAAGAACCAAGGATGATGAGATGTTACCCCTGCCGCT 658  
 Db 684 GTCTTTTCAAAAAGTGTGCAAGAACCAACCAATAGGCCCCCCCCCAAGACGGA- 742  
 QY 659 CGACGCAAGATCCCCAGGAGATGAAGATTATCCCGTCTATAACACCGTCTCTCCAGTG 718  
 Db 743 --ACCCAGGAGATCAATTTTCCGACGATCTTCTGCTCCAACTGCTGCTCCAGTG 800  
 QY 719 CAGGAGACACTGCGGCTGTGAGCTGTACAGGAGGATGTTAAGAGAGTTCGCATC 778  
 Db 801 CAGGAGACTTTACATGGATGCCAACCGCTCACCCAGGAGGATGGCAAGAGTTCGCATC 860  
 QY 779 TCAGTGCAGGAGCGGCAG 796  
 Db 861 TCAGTGCAGGAGAGACAG 878

RESULT 10  
 AAV63454  
 ID AAV63454 standard; cDNA; 1004 BP.  
 XX  
 AC AAV63454;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-JUN-1999 (first entry)  
 XX  
 DE Human CD40 antigen cDNA.  
 XX  
 KW CD40; cell surface antigen; T cell antigen; T lymphocyte; human; cloning;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5830731-A.  
 XX  
 PD 03-NOV-1998.  
 XX  
 XX 21-MAY-1997; 97US-00861205.  
 PF  
 XX 25-FEB-1988; 88US-00160416.  
 PR 13-JUL-1989; 89US-00379076.  
 PR

PR	23-MAR-1990;	90US-00498809.	
PR	13-JUL-1990;	90US-00553759.	
PR	01-DEC-1992;	92US-00983647.	
XX			
XX	(GEO ) GEN HOSPITAL CORP.		
XX			
PI	Seed B, Aruffo A;		
XX			
XX	WPI; 1998-609251/51.		
XX			
PT	New cloning vector and poly:linker - based on existing sequences for		
PT	efficient cloning and expression of mammalian cDNA(s), especially human		
PT	lymphocyte antigenic sequences.		
XX			
XX	Example 8; Fig 16; 75pp; English.		
PS			
XX			
CC	This nucleotide sequence comprises human CD40 antigen cDNA. It was		
CC	isolated by a novel method for cloning cDNAs from mammalian expression		
CC	libraries that is based on transient expression of an antigen in		
CC	eukaryotic cells and physical selection of cells expressing the antigen		
CC	by adhesion to an antibody-coated substrate, such as a culture dish. The		
CC	method is useful for the isolation and molecular cloning of any protein		
CC	which can be expressed and transported to the cell surface membrane of a		
CC	eukaryotic cell. It has been used to clone genes (see AAU63442-63)		
CC	encoding cell surface antigens from mammalian lymphocytes (see AAU80440-		
CC	55). The isolated genes can be expressed in a prokaryotic or eukaryotic		
CC	host cells to produce the encoded protein. The invention also provides		
CC	high efficiency expression vectors (see AAU63441 and AAU63444) which		
CC	allow the generation of very large mammalian expression libraries. The		
CC	purified genes and proteins are useful for immunodiagnostic and		
CC	immunotherapeutic applications, including the diagnosis and treatment of		
CC	immune-mediated infections, diseases, and disorders of animals, including		
CC	humans. (Updated on 25-MAR-2003 to correct PR field.)		
XX			
SQ	Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;		
	Query Match 34.7%; Score 280.4; DB 2; Length 1004;		
	Best Local Similarity 62.7%; Pred. No. 3.9e-79;		
	Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3		
QY	1	ATGGTGTCCTTTGCCCTCGGCTGTGCGCGTATGGGGCTGCTTTGTGACAGGGTCCATCTA	60
Db	48	ATGGTTCTGCTGCCCTCTGCAGTGTGGTGTCTCTGGGGCTGCTTGTGACCGTGTCCATCCA	107
QY	61	GGCGAGTGTGTTACTGTGCAGTGACAAACAGTACTCCACGATGGCCAGTCTGTGATTTG	120
Db	108	GAACACCCACCTGCATGTCAGAGAAACACGTACCTAATAACAGTCAGTCTGTTCTTTG	167
QY	121	TGCCAGCCAGGAGCGGACTGACAGCCACTGCACAGCTCTTGAGAGACCCCAATGCCAC	180
Db	168	TGCCAGCCAGGAGCAGAACTGTGTGAGTACTGTGCACAGATTCTAGAACGGGAATGCC	227
QY	181	CCATGTGACTCAGGGCGAAATTCCTAGCCCAAGTGGAAACAGGAGAGATTGCTGTTCAC	240
Db	228	CCTTGGCGGTAAAGCGAATTCCTAGACACCTGGAAACAGAGAGACACATGCCAC	287
QY	241	AGACACTGTGAACCCAGTGCCTGGGGCTGCTCGGGAAGGATCAAGGGCTTCGGGTAA	300
Db	288	AAATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCCAG	323
QY	301	AAGGAGGGGACCGCAGAAATCAGACACTGTCTGTACTCTGAAGGAAGACAACTGCACC	360
Db	324	CAGAGGGGACCTCAGAAACAGACACCACTCTGCACCTGTGAAGAGCTGGCACTGTAG	383
QY	361	AGCAAGGATTCGAGCGCATGTGCTCAGACACAGCCCTGTATCCCTGGCTTTGGAGTTAT	420
Db	384	AGTGAGGGCCTGTGAGAGCTGTGTCTGTGACCCGCTCATGCTCGCCCGCTTTGGGGT	443
QY	421	GAGATGGCCACTGAGACCACTGATACCGTGTGTATCCCTGGCCAGTTCGGCTTCTTCC	480
Db	444	CAGATTGCTACAGGGGTTTCTGTATACCAATCTGCGAGCCCTGCCCAGTTCGGCTTCTT	503
QY	481	AATCAGTCAATCACTTTTCGAAAGTGTGTATCCCTGGACAAAGGTTTAA-----	527

CC according to defined criteria. Also described are: (1) a method of  
CC defining a set of oligonucleotides (ONs) that modulate the expression of  
CC a tNA sequence via binding of the ONs with the tNA sequence comprising  
CC generating a library of virtual compounds in silico according to defined  
CC criteria, and evaluating in silico the binding of the virtual ONs with  
CC the tNA according to defined criteria; and (2) a method of defining a set  
CC of compounds that modulate the expression of a tNA sequence via binding  
CC of the compounds with the tNA. The methods can be used for the generation  
CC and identification of synthetic compounds having defined physical,  
CC chemical or bioactive properties. Information gathered from assays of  
CC such compounds is used to identify nucleic acid sequences that are  
CC tractable to a variety of nucleotide sequence-based technologies, e.g.,  
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and  
CC AAY52701 to AAY52706, represent sequences used in the exemplification of  
CC the present invention

XX Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

Query Match 34.7%; Score 280.4; DB 2; Length 1004;

Best Local Similarity 62.7%; Pred. No. 3.9e-79;

Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;

QY 1 ATGTGCTCTTTCCTCGGCTGTGCGCGCTATGGGCTGCTGTGTTGACAGCGGTCCATCTA 60  
DB |||||  
QY 48 ATGTGCTCTTTCCTCGGCTGTGCGCGCTATGGGCTGCTGTGTTGACAGCGGTCCATCTA 107  
DB |||||  
QY 61 GGGCAGTGTGTACGTGCGTGAACAACAGTACCTCCACGATGCCAGTCTGTGATTTG 120  
DB |||||  
QY 108 GAACACCCACTGATGAGAGAAAACAGTACCTTAATAACAGTCTGTGCTGTTT 157  
DB |||||  
QY 121 TGCCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTCTTGAGAGACCCCAATGCCAC 180  
DB |||||  
QY 168 TGCCAGCCAGGACAGAAACTGGTGAAGTGACTGCACAGAGTTCACTGAACCGAATGCCIT 227  
DB |||||  
QY 181 CCATGTGACTCAGCGAATCTCAGCCAGTGGACAGGAGATTCCTGTCTACCCAGCAC 240  
DB |||||  
QY 228 CTTTGGCGGTGAAGCGAATTCCTAGACACCTTGGAAACAGAGACACACTGCCACACGAC 287  
DB |||||  
QY 241 AGACACTGTGAACCCAGCTGCGTGGGGTGTCTGGGAAGGGATCAAGGGCTTCGGGTAAAG 300  
DB |||||  
QY 288 AATGCTGGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323  
DB |||||  
QY 301 AAGAGGGCCAGGAGATCAGACATGTCTGTACCTGTGTAAGGAGACAACTGCAC 360  
DB |||||  
QY 324 CAGAAGGGCCACTCAGAAACAGACACCATCTGCACCTGTGTAAGAGGCTGGCACTGTACG 383  
DB |||||  
QY 361 AGCAAGGATTCGAGGATGTGCTCAGACACGCGCTGTATCCTGCTGTGGAGTTATG 420  
DB |||||  
QY 384 AGTGAGGCTGTGAGAGCTGTGCTCGACCGCTCATGCTCGCCGCTTTGGGTCAAG 443  
DB |||||  
QY 421 GAGATGGCCATGAGACATGATACCGTGTGTATCCTGCGCCAGTCGCTCTCTCTCC 480  
DB |||||  
QY 444 CAGATGTGTACAGGGGTTCTGTATACCATCTGCGAGCCCTGCCAGTCGCGCTCTCTCTCC 503  
DB |||||  
QY 481 AATCAGTCACTACTTTCGAAAGTGTATCCCTGGACAAGGTTTA-----527  
DB |||||  
QY 504 AATGTGTATCTGCTTTTCGAAAATGTACCCCTTGGAAAGCTGTGAGACCAAGACCTG 563  
DB |||||  
QY 528 -----AGTCCCGGATG 538  
DB |||||  
QY 564 GTTGTGCAACAGGCGGACAAACAGACTGATGTTGTGTGTGTCGCCAGGATCGCGTG 623  
DB |||||  
QY 539 CGAGCCCTGCTGTCATCTCTGTGTCGTGATGGGATCTCTATCCATTTTCGGGGTGT 598  
DB |||||  
QY 624 AGAGCCCTGGTGGTATCCCATCATCTTGGGATCTGTTTGGCATCTCTTGTGGTCTG 683  
DB |||||  
QY 599 CTCTATATCAAAAAGGTGGTCAAGAAACCAAGGATATGAGATGTTTACCCCTCGGGCT 658  
DB |||||  
QY 684 GTCTTTATCAAAAAGGTGGGCAAGAGACCAACCAATGAGCCGCCCCCAAGCAGGA- 742  
DB |||||  
QY 659 CGAGGGCAGATCCCGAGGAGATGGAAGATATCCCGGTATACACCGCTGTCTCCAGTG 718  
DB |||||  
QY 743 --ACCCCGAGGAGATCAATTTTCCCGAGGATCTCTCGCTCCCAACACTGCTGTCCAGTG 800  
DB |||||

QY 719 CAGGAGCACTGCACGGGTGTACGCTGTACACAGGAGGATGCTAAAGAGATCGCATC 778  
DB |||||  
QY 801 CAGGAGATTTTACATGGATGCCAACCGGTACCCAGGAGGATGGCAAGAGATCGCATC 860  
DB |||||  
QY 779 TCAGTGCAGGAGCGCGCAG 796  
DB |||||  
QY 861 TCAGTGCAGGAGAGACAG 878  
DB |||||

RESULT 12

AAV81198

ID AAV81198 standard; cDNA; 1004 BP.

XX AAV81198;

XX

DT 10-MAY-1999 (first entry)

XX

DE Human CD40 antigen cDNA.

XX

KW CD40; cell surface antigen; T cell antigen; T lymphocyte; human;

XX cDNA library; ss.

XX

OS Homo sapiens.

XX

PN US5849898-A.

XX

PD 15-DEC-1998.

XX

PF 07-JUN-1995; 95US-00485447.

XX

PR 25-FEB-1988; 88US-00160416.

PR

PR 13-JUL-1989; 89US-00379076.

PR

PR 23-MAR-1990; 90US-00498809.

PR

PR 13-JUL-1990; 90US-0053759.

PR

PR 01-DEC-1992; 92US-00983647.

XX

PA (GEO) GEN HOSPITAL CORP..

XX

PI Seed B, Oquendo C, Camerini D, Stamenkovic I, Stengelin S;

PI Amiot M, Lauffer L, Allen J, Simmons D, Aruffo A;

XX

DR WPI; 1999-069813/06.

XX

XX cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell

XX surface antigens, constructing cDNA libraries, expressing vectors for

XX expression in eukaryotic cells or their fragments.

PT

PS Claim 2; Fig 16; 79pp; English.

XX

CC This nucleotide sequence comprises human CD40 antigen cDNA. It was  
CC isolated by a novel method for cloning cDNAs from mammalian expression  
CC libraries that is based on transient expression of an antigen in  
CC eukaryotic cells and physical selection of cells expressing the antigen  
CC by adhesion to an antibody-coated substrate, such as a culture dish. The  
CC method is useful for the isolation and molecular cloning of any protein  
CC which can be expressed and transported to the cell surface membrane of a  
CC eukaryotic cell. It has been used to clone genes (see AAV81198-220)  
CC encoding cell surface antigens such as CD1a, CD1b, CD1c, CD2, CD6, CD7,  
CC CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27, CD28, CD31, CD32a,  
CC CD32b, CD33, CD34, CD36, CD37, CD38, CD39, CD40, CD43, CD44, CD53, ICAM,  
CC LFA-3, FCRII, FCRIIb, T11a and Leu8 (see AAW86188-62, AAW89151-52 and  
CC AAW88451). The isolated genes can be expressed in a prokaryotic or  
CC eukaryotic host cell to produce the encoded protein. The invention also  
CC provides high efficiency expression vectors which allow the generation of  
CC very large mammalian expression libraries

XX Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

XX

Query Match 34.7%; Score 280.4; DB 2; Length 1004;

Best Local Similarity 62.7%; Pred. No. 3.9e-79;

Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;

```
QY 1 ATGGTGTCTTTGCTGGCTGTGCGCGTATATGGGCTGCTTGTGACAGCGTCCATCTA 60
DQ |||||
DB 48 ATGGTTCGTCTGCTCTGCGAGTGGCTCTCTCTGGGCTGCTTCTGACCGTCTCCATCCA 107
QY 61 GGGCAGTGTGTACGTGCTGCTGACAAACAGTACTCCACGATGGCAGTGTGTGTTG 120
DB |||||
DB 108 GAACACCCACTGCAATGCGAGAAAACAGTACCTTAATAACAGTCAGTGTGTCTTTG 167
QY 121 TGCACCGCAGGAGCGCACTGCAAGCCACTGCACAGCTCTTGAGAAGACCCCAATGCCAC 180
DB |||||
DB 168 TGCCAGCCAGGACAGAACTGCTGAGTGACTGCACAGAGTTCACCTGAACGGAATGCCTT 227
QY 181 CATGTGACTCAGGCGAATCTCAGCCAGTGTGAACAGGAGATTCGCTGTCCACGAC 240
DB |||||
DB 228 CCTTGGCGTGAAGCGAATCTCTAGACACCTGGAACAGAGACACACTGCCACACGAC 287
QY 241 AGACACTGTGAACCCAGTGGCTGCTGGGAGGGAATCAAGGGCTTCGGGTAAAG 300
DB |||||
DB 288 AATACTGGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323
QY 301 AAGAGGGCAGCGCAGAACTCAGACACTGTCTGTACTGTGAAGAGGACAACTGCAC 360
DB |||||
DB 324 CAGAGGGCACCTTCAGAAACAGACACCACTCTGCACCTGTGAAGAGGCTGGCACTGTAC 383
QY 361 AGCAAGGATTGGAGCATGTCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG 420
DB |||||
DB 384 AGTAGGCTGTGAGAGCTGTCTGACCCGCTCATGCTCGCCGCTTTGGGTCAG 443
QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTCTATCCCTGCCAGTGGCTTCTTCC 480
DB |||||
DB 444 CAGATTGCTACAGGGTCTTCTGATACCACTCTGGAGCCCTGCCAGTGGCTTCTTCC 503
QY 481 AATCAGTCATCTTTTGAAGAGTGTATCCCTGGACAAAGTTTAA----- 527
DB |||||
DB 504 AATGTCTCATCTGCTTTTCGAAAATGTCACTCTGGACAAAGTGTGAGACCAAGACCTG 563
QY 528 -----AGTCCCGGATG 538
DB |||||
DB 564 GTTGTGCACAGGACGACCAACAGACTGATGTGTGTGTTCCCGAGATCGGCTG 623
QY 539 CGAGCCCTGCTGTCATCTCTGTGTGATGGGATCTCATCACCATTCTGGGCTGTTT 598
DB |||||
DB 624 AGAGCCCTGCTGATCCCATCTCTCTGGGATCTCTTTGCCATCTCTTGTGTGCTG 683
QY 599 CTCTATATCAAAAGTGTGCAAGAACCAAGGATAATGAGATGTACCCCTCGGCT 658
DB |||||
DB 684 GTCTTATCAAAAGTGGCCAAAGAACCAACCAATGAGGCCCTCCACCCCAAGCAGGA- 742
QY 659 CGACGGCAAGATCCCGAGGATGGAAGATTATCCCGGTATATACACACCGCTCTCCAGTG 718
DB |||||
DB 743 --ACCCAGGAGATCAATTTTCCGACGATCTCTGCTGCTCCACACTGCTCTCCAGTG 800
QY 719 CAGGACACTGACCGGTGTGAGCTGTCAACAGGAGATGTTAAGAGATGCGATC 778
DB |||||
DB 801 CAGGAGACTTTATCATGATGCCAACCGGTGATCCCGTACCCAGGAGATGGCAAGAGATGCGATC 860
QY 779 TCAGTGCAGGAGCGGAG 796
DB |||||
DB 861 TCAGTGCAGGAGACAG 878
```

## RESULT 13

```
AA223432
ID AA223432 standard; DNA; 1004 BP.
```

AC AA223432;

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

atrophin-1; cell death; apoptosis; Huntington's disease; head trauma; Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke; dentatorubropallidoluysian atrophy; cell proliferation; cell survival; neoplastic; malignant; autoimmune; fibrotic; CD40; ss.

Homo sapiens.

Key	Location/Qualifiers
FT	48..881
FT	/*tag= a
FT	/product= "CD40"

W09945944-A1.

16-SEP-1999.

11-MAR-1999; 99WO-US005250.

12-MAR-1998; 98US-00041886.

(BURN-) BURNHAM INST.

Bredesen DE, Rabizadeh S;

WPI; 1999-561617/47.

P-PSDB; AAY33499.

New proapoptotic dependence peptides, used to develop products for treating, e.g. Alzheimer's disease.

Disclosure; Page 168-169; 199pp; English.

This invention describes novel pure proapoptotic dependence peptides which comprise a sequence of an active dependence domain selected from dependence polypeptides consisting of p75NTR, androgen receptor, DCC, huntingtin polypeptide, Machado-Joseph disease gene product, SCAL, SCA2, SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of inducing cell death and can be used to develop products to mediate or inhibit apoptosis. The methods can be used for reducing the severity of a proapoptotic dependence domain mediated pathological conditions e.g. Huntington's disease, Alzheimer's disease, Kennedy's disease, Machado-Joseph disease, stroke or head trauma. They can also be used for reducing the severity of a pathological condition mediated by upregulated cell proliferation or cell survival e.g. neoplastic, malignant, autoimmune or fibrotic conditions. This sequence encodes the human CD40 polypeptide described in the method of the invention

Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

Query Match 34.7%; Score 280.4; DB 2; Length 1004;

Best Local Similarity 62.7%; Pred. No. 3.9e-79;

Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;

QY 1 ATGGTGTCTTTGCTGGCTGTGCGCTATATGGGCTGCTTGTGACAGCGTCCATCTA 60

DB 48 ATGGTTCGTCTGCTCTGAGTGGCTCTCTGGGCTGCTTGTGACCGTGTCCATCCA 107

QY 61 GGGCAGTGTGTACGTGCGATGACAAACAGTACCTCCACGATGCCAGTGTGTGATTG 120

DB 108 GAACACCCACTGTCATGACAGAGAAAACAGTACCTTAATACACTGCTGTCTTTG 167

QY 121 TGCCAGCCAGGAAGCCGACTGACAAAGCCACTGCACAGCTTTGAGAAGACCAATGCCAC 180

DB 168 TGCCAGCCAGGACAGAAAACCTGGTGTGCTGCTGACAGAGTTCACCTGAACCGAATGCCTT 227

QY 181 CCATGTGACTCAGGGAATCTCAGCCAGTGGGAGGAGATTCCTGTCTCACCAGCAC 240

DB 228 CCTTGGCGTGAAGCGAATTCCTAGACACCTGGAACAGAGACACACTGTCACAGCAC 287

QY 241 AGACACTGTGAACCCAGTGGCTGCTGGGAGGATCAAGGCTTCGGGTAAAG 300

DB 288 AATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323

Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC; huntingtin polypeptide; Machado-Joseph disease; SCAL; SCA2; SCA6;

QY 301 AAGAGGGCCACCGAGAAATCAGACATGCTGTCTGTACCTGTGTAAGGAGGACAACTGCACC 360  
 Db 324 CAGAAGGGCCACCTCAGAAACAGACACCATCTGCACCTGTGAAGAGGCTGGCACTGTACG 383  
 QY 361 AGCAAGGATTCGAGGATGTGCTCAGACACGCGCTGTATCCCTGGCTTTGAGATTATG 420  
 Db 384 AGTAGGGCTGTGAGAGTGTCTCTGACCGCTCATGCTGCGCGGCTTTGGGTCAG 443  
 QY 421 GAGATGGCCACTGAGACACATGATACCGTGTGTATCCCTGCCAGTCGGCTTTCTCTCC 480  
 Db 444 CAGATTGCTACAGGGGTTCTGTATACCATCTGCGAGCCCTGCCAGTCGGCTTTCTCTCC 503  
 QY 481 AATCAGTATCATCTTTTCGAAAAGTGTATCCCTGGACAGGTTTAA-----527  
 Db 504 AATGTGTATCTGCTTTTCGAAAATGTATCCCTTTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 Db 564 GTTGTGCAACAGGAGGACCAACAGACTGATGTTGTCTGTGTCCTCCAGGATCGGCTG 623  
 QY 539 CGAGCCCTGCTGTCATCTCTGTCGTGATGGGATCCTCATCACCATTTCGGGGTGT 598  
 Db 624 AGAGCCCTGGTGGTATCCCATCATCTTCGGGATCCTGTTGCCATCTCTTTGGTGTG 683  
 QY 599 CTCTATATCAAAAAGGTGGTCAAGAAACCAAGAGATATAGATGTTTACCCCTCGGGCT 658  
 Db 684 GTCTTTATCAAAAAGGTGGTCAAGAAACCAAGAGATATAGAGTAAAGCCCTCCAGCAGGA- 742  
 QY 659 CGAGGCAAGATCCCGAGGAGATGGAAGATTATCCCGGTATACACCGCTGTCTCAGTG 718  
 Db 743 --ACCCGAGGAGATCAATTTTCCCGAGGATCTTCTCGGCTCCAACTGCTGTCTCAGTG 800  
 QY 719 CAGGAGACACTGCACGGGTGTCAGCCTGTACACAGGAGGATGTAAGAGAGTCCGATC 778  
 Db 801 CAGAGACTTTACATGATGCAACCGGTACCCAGGAGGATGGCAAGAGAGTCCGATC 860  
 QY 779 TCAGTCAGGAGCGGCAG 796  
 Db 861 TCAGTCAGGAGAGACAG 878

RESULT 14  
 AAA50590  
 ID AAA50590 standard; cDNA; 1004 BP.  
 XX AC AAA50590;  
 XX DT 19-DEC-2000 (first entry)  
 XX DE Human cell surface antigen CD40 cDNA.  
 XX KW CD40; cell surface antigen; human; immunoselection; panning;  
 XX KW immunodiagnosis; diagnosis; immunotherapy; gene therapy; immune disorder;  
 XX KW infection; asthma; immune-complex disease; amyloidosis;  
 XX KW multiple sclerosis; parasitic disease; ss.  
 XX OS Homo sapiens.  
 XX PN US6111093-A.  
 XX PD 29-AUG-2000.  
 XX PP 28-OCT-1998; 98US-00181612.  
 XX PR 25-FEB-1988; 88US-00160416.  
 XX PR 13-JUL-1989; 89US-00379076.  
 XX PR 23-MAR-1990; 90US-00498809.  
 XX PR 13-JUL-1990; 90US-00553759.  
 XX PR 01-DEC-1992; 92US-00983647.  
 XX PA (GEHO ) GEN HOSPITAL CORP.  
 XX

PI Stamenkovic I, Seed B;  
 XX WPI; 2000-586382/55.  
 XX  
 PT Isolated nucleic acid molecule encoding the CD19 cell surface antigen,  
 PT useful for immunodiagnosis and immunotherapy of immune-mediated  
 PT infections or disorders, e.g. asthma, immune-complex disease, parasitic  
 PT diseases.  
 XX  
 PS Claim 1; Fig 16; 75pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human cell surface antigen  
 CC (CSA) CD40. The cDNA was isolated using a rapid immunoselection cloning  
 CC method of the invention, designed to isolate CSA cDNAs. The method is  
 CC based upon transient expression of a CSA in eukaryotic cells and physical  
 CC selection of cells expressing the antigen by adhesion to (panning on) an  
 CC antibody-coated substrate such as a culture dish. CSA nucleic acids  
 CC isolated by the method of the invention, and the proteins they encode,  
 CC are useful for immunodiagnosis and immunotherapeutic applications,  
 CC including the diagnosis and treatment of immune-mediated infections,  
 CC diseases, and disorders in animals, including humans. These disorders  
 CC include asthma, immune-complex disease, amyloidosis, parasitic diseases  
 CC or multiple sclerosis  
 XX  
 SQ Sequence 1004 BP; 230 A; 287 C; 276 G; 201 T; 0 U; 0 Other;  
 Query Match 34.7%; Score 280.4; DB 3; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;  
 QY 1 AFGGTGTCTTTGCTCGGCTGTGCGCTATGGGGCTGCTTGTGACAGCGTCCATCTA 60  
 Db 48 ATGGTTCGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107  
 QY 61 GGGCAGTGTGTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 108 GAACACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 167  
 QY 121 TGCCAGCCAGGAGCCGACTGACAGCCACTGACAGCTCTTGAGAGACCAATGCAC 180  
 Db 168 TGCCAGCCAGGAGCAGAACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 227  
 QY 181 CCATGTGACTCAGCGGATCTCAGCCAGTGGAGAGGAGATTCGCTGTCACCGAC 240  
 Db 228 CCTTGGGTGAAAGCGAATCTTAGACACCTGGAGACAGAGAGACACACTGCCACAGAC 287  
 QY 241 AGACACTGTGAACCCAGTGCCTGGGGCTGCTGCGGAGGATCAAGGGCTTCGGGTAAAG 300  
 Db 288 AATATCTCGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323  
 QY 301 AAGGAGGCGACCGAGATCAGACACTGTCTGTACCTGTGTAAGGAGGACACACTGCACC 360  
 Db 324 CAGAAGGGCCACCTCAGAAACAGACACCATCTGCACCTGTGAAGAGGCTGGCACTGTACG 383  
 QY 361 AGCAAGGATTCGAGGATGTGCTCAGACACGCGCTGTATCCCTGGCTTTGAGATTATG 420  
 Db 384 AGTAGGGCTGTGAGAGTGTCTCTGACCGCTCATGCTGCGCGGCTTTGGGTCAG 443  
 QY 421 GAGATGGCCACTGAGACACATGATACCGTGTGTATCCCTGCCAGTCGGCTTTCTCTCC 480  
 Db 444 CAGATTGCTACAGGGGTTTCTGTATACCATCTGCGAGCCCTGCCAGTCGGCTTTCTCTCC 503  
 QY 481 AATCAGTATCATCTTTTCGAAAAGTGTATCCCTGGACAGGTTTAA-----527  
 Db 504 AATGTGTATCTGCTTTTCGAAAATGTATCCCTTTGGACAGCTGTGAGACCAAGACCTG 563  
 QY 528 -----AGTCCCGGATG 538  
 Db 564 GTTGTGCAACAGGAGGACCAACAGACTGATGTTGTCTGTGTCCTCCAGGATCGGCTG 623  
 QY 539 CGAGCCCTGCTGTCATCTCTGTCGTGATGGGATCCTCATCACCATTTCGGGGTGT 598  
 Db 624 AGAGCCCTGGTGGTATCCCATCATCTTCGGGATCCTGTTGCCATCTCTTTGGTGTG 683

599 CTCATATCAAAAGGTGCTCAAGAAACCAAGGATAATGAGATGTACCCCTCGGCT 658  
 684 GTCCTTATCAAAAGGTGCTCAAGAAACCAATAGCCCTCCCAAGCAGA- 742  
 659 CGAGCGCAAGATCCCGAGAGATGGAATATCCGGTCATAACACCGCTGCTCCAGT 718  
 743 --ACCCAGGAGATCAATTTTCCGACGATCTTCTGGTCCCAACACTGCTCCAGT 800  
 719 CAGGAGACACTGCACGGGTGCTAGCTGTACACACAGGAGATGTTAAAGAGATGCGATC 778  
 801 CAGGAGACTTTACATGGATGCCAACCGGTACCCAGAGATGGCAAGAGAGTGCATC 860  
 779 TCAGTCAGGAGCGGAG 796  
 861 TCAGTCAGGAGACAG 878

RESULT 15  
 AA247769  
 ID AA247769 standard; DNA; 1004 BP.  
 XX  
 AC AA247769;  
 XX  
 DT 02-MAR-2000 (first entry)  
 XX  
 DE Human CD40 nucleotide sequence SEQ ID NO:85.  
 XX  
 KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;  
 KW expression; immune disease; inflammatory disease; immunomodulatory;  
 KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;  
 KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;  
 KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;  
 KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO957320-A1.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 22-APR-1999; 99WO-US008765.  
 XX  
 PR 01-MAY-1998; 98US-00071433.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowser LM;  
 XX  
 DR WPI; 2000-062158/05.  
 XX  
 PT Antisense molecules directed against nucleic acid encoding human CD40,  
 PT for treating e.g. immune, inflammatory or hyperproliferative diseases.  
 XX  
 PS Example 9; Page 97-98; 102pp; English.  
 XX  
 CC AA247768 to AA247769 represent phosphorothioate antisense  
 CC oligonucleotides targeted to human CD40, which can be used to inhibit the  
 CC expression of human CD40. CD40 is involved in lymphocyte activation,  
 CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or  
 CC prevent immune-associated diseases (specifically guest vs. host disease,  
 CC allograft rejection or autoimmune diseases); inflammation (specifically  
 CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel  
 CC disease or psoriasis) or hyperproliferation (specifically cancer and  
 CC tumours). the antisense oligonucleotides are also useful as diagnostic  
 CC and research reagents. AA247769 represents the human CD40 nucleotide  
 CC sequence. AA247770 to AA247772 represent human CD40 forward and reverse  
 CC PCR primers, and a human CD40 PCR probe, respectively. AA247773 to  
 CC AA247775 represent other PCR primers and a probe used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

Query Match 34.7%; Score 280.4; DB 3; Length 1004;  
 Best Local Similarity 62.7%; Pred. No. 3.9e-79;  
 Matches 538; Conservative 0; Mismatches 231; Indels 89; Gaps 3;

QY 1 ATGTGTTCTTTGGCTCGGCTGTGGCGCTATGGGCTGCTTTGTGACAGCGGTCCATCTA 60  
 Db 48 ATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 107  
 QY 61 GGGCAGTGTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 108 GAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 167  
 QY 121 TGCAGCAGGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 Db 168 TGCAGCAGGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 227  
 QY 181 CCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 228 CTTGCGGTGAGCGAATTTCTGAGACACCTGGAACAGAGAGACACTGCTGCTGCTGCTGCTGCT 287  
 QY 241 AGACACTGTGAAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 Db 288 AATACTGCGACCCCA-----ACCTAGGGCTTCGGGTCCAG 323  
 QY 301 AAGGAGGCGCCGAGAACTGAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 Db 324 CAGAAGGCGCACTCAGAAACAGACACCATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 383  
 QY 361 AGCAAGGATTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
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 QY 421 GAGATGGCTGCTGAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
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 QY 481 AATCAGTCACTCACTTTTCGAAAGCTTATCCCTGGAAGGTTTAA----- 527  
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 QY 528 -----AGTCCCGGATG 538  
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 Db 624 AGAGCCTGCT 683  
 QY 599 CTCTATATCAAAAGGTGCTCAAGAAACCAAGGATAATGAGATGTTTACCCCTCGGCT 658  
 Db 684 GTCCTTATCAAAAGGTGCTCAAGAAACCAAGGATAATGAGATGTTTACCCCTCGGCT 742  
 QY 659 CGAGCCTGCT 718  
 Db 743 --ACCCAGGAGATCAATTTTCCCGACGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800  
 QY 719 CAGGAGACTGCT 778  
 Db 801 CAGGAGACTTTACATGGATGCCAACCGGTACCCAGAGATGGCAAGAGAGTGCATC 860  
 QY 779 TCAGTCAGGAGCGGAG 796  
 Db 861 TCAGTCAGGAGACAG 878

Search completed: July 25, 2004, 01:05:53  
 Job time : 404 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 24, 2004, 23:50:12 ; Search time 2499 Seconds

(without alignments)

9667.269 Million cell updates/sec

Title: US-10-031-607-6

Perfect score: 809

Sequence: 1 atgggtgtcttgcctcggtc.....gcggcaggtgacagacagca 809

Scoring table:

IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_estcl.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rcd.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gssl.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	679	93.9	2901	11	AK089861 Mus muscu
2	670	92.8	947	13	BU516152 AGENCOURT
3	494.8	61.2	692	13	BY751423 BY751423
4	467	57.7	663	13	BY743050 BY743050

5	464.6	57.4	647	13	BY745486
6	464.6	57.4	665	13	BY751441
7	463.6	57.3	649	13	BY744299
8	448.4	55.4	655	13	BY745292
9	444.6	55.0	941	10	BF166137
10	443.6	54.8	656	13	BY745260
11	380.6	47.0	603	14	CB547441
12	377.4	46.6	440	13	BY211683
13	370.4	45.8	435	13	BY0411398
14	355.4	43.9	429	13	BY211594
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16	344.2	42.5	409	13	BY211153
17	343.8	42.5	433	13	BY211500
18	343	42.4	390	13	BY212394
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24	334.2	41.3	418	13	BY217907
25	332	41.0	396	13	BY164847
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27	328.2	40.6	399	13	BY218151
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29	320.8	39.7	416	13	BY165294
30	320.4	39.6	397	13	BY058815
31	319.6	39.5	545	12	EG276290
32	318.4	39.4	385	13	BY165017
33	316	39.1	376	13	BY160241
34	312.8	38.7	469	9	AI385482
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#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830034E13 product: Tumor necrosis factor receptor superfamily member 5, full insert sequence.  
ACCESSION AK089861  
VERSION AK089861.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

2901 bp mRNA linear HTC 20-SEP-2003  
Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830034E13 product: Tumor necrosis factor receptor superfamily member 5, full insert sequence.

AK089861.1 GI:26354702  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

```

3
REFERENCE
AUTHORS
  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
  Konno,H., Akiyama,O., Nishi,K., Kitesunai,T., Rashiro,H., Itoh,M.,
  Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
  Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
  Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
  Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J.,
  Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE
  RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL
MEDLINE
  Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
  11076861
REFERENCE
AUTHORS
4
  The RIKEN Genome Exploration Research Group Phase II Team and the
  PANTOM Consortium.
TITLE
  Functional annotation of a full-length mouse cDNA collection
JOURNAL
MEDLINE
  Nature 409, 685-690 (2001)
PUBMED
  11076861
REFERENCE
AUTHORS
5
  The PANTOM Consortium and the RIKEN Genome Exploration Research
  Group Phase I & II Team.
TITLE
  Analysis of the mouse transcriptome based on functional annotation
  of 60,770 full-length cDNAs
JOURNAL
MEDLINE
  Nature 420, 563-573 (2002)
PUBMED
  12000000
REFERENCE
AUTHORS
  Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
  Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
  Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
  Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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  Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
  Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
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  Takeda,Y., Tanaka,T., Tonari,A., Toya,T., Yasunishi,A.,
  Muramatsu,M. and Hayashizaki,Y.
TITLE
  Direct Submission
JOURNAL
MEDLINE
  Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
  Physical and Chemical Research (RIKEN), Laboratory for Genome
  Exploration-Research Group, RIKEN Genomic Sciences Center (GSC),
  RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
  Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp,
  URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
  Fax:81-45-503-9216)
COMMENT
  cDNA library was prepared and sequenced in Mouse Genome
  Encyclopedia Project of Genome Exploration Research Group in Riken
  Genomic Sciences Center and Genome Science Laboratory in RIKEN.
  Division of Experimental Animal Research in Riken contributed to
  prepare mouse tissues.
  Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
  Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
  Trust/MRC building Addenbrookes Hospital Cambridge) whose
  assistance we gratefully acknowledge.
  Please visit our web site for further details.
  URL:http://genome.gsc.riken.go.jp/
  URL:http://fantom.gsc.riken.go.jp/.
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    Best Local Similarity 90.1%; Pred. No. 1.2e-196;
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  QY 61 GGGCAGTGTGTACGTGAGTGACAAAAGTACCTCCAGATGGCCAGTGTGTGATTG 120
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  QY 121 TCCAGAGCAGAGCCGACTGACAGCCACTGCACAGCTCTTGAGAGACCAATGCCAC 180
  Db 146 TCCAGAGCAGAGCCGACTGACAGCCACTGCACAGCTCTTGAGAGACCAATGCCAC 205
  QY 181 CCATGTGACTCAGCGCAATTTCTAGCCCAAGTGGAAACAGGGAGATTCCTGTGACACGAC 240
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  QY 241 AGACACTGTGAACCCAGTGGCTGGGGCTGCTGGAGAGGATCAAGGCTTCGGGTTAAG 300
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IMAGE:6512860 5', mRNA sequence.
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VERSION BUS16152.1 GI:22823678
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 947)
TITLE NIH-MGC http://mgi.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14085 row: k column: 05
High quality sequence stop: 723.
FEATURES
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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/notes="Vector: PCMV-SPO76.1; Site 1: EcoRV; Site 2: NotI;
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size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 82.8%; Score 670; DB 13; Length 947;
Best Local Similarity 89.4%; Pred. No. 3.6e-194; Mismatches 6; Indels 86; Gaps 2;
Matches 779; Conservative 0;
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DB 245 AGACACTGTGAACCCCA-----ATCAGGGGCTTCGGGTAAAG 280
QY 301 AAGAGGGGCAACCGCAGAAATCAGACACTGTCTGTACCTGTGAAGGAAGGCAACACTGCACC 360
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DB 821 TCANTGAGGAGCGGCGAGGTGACAGACAGCA 851
RESULT 3
LOCUS BY751423
DEFINITION BY751423 RIKEN full-length enriched, activated spleen Mus musculus
cDNA clone F830034E13 5', mRNA sequence.
ACCESSION BY751423
VERSION BY751423.1 GI:27181814
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 692)
QY 1 ATGGTGCTCTTTCCTCGGCTGTGCGCGCTATGCGGCTGCTTGTTCACAGCGGTCCTCATCTA 60
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QY 361 AGCAAGGATTGGAGGCAATGTGCTCAGCACAGCCCTGTATCCCTGGCTTTGGAGTTATG 420
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sakai, D., Sasaki, K., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)  
MEDLINE 22354683  
PUBMED 12468851  
COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Inctani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, K., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

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/mol\_type="mRNA"

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/db\_xref="taxon:10090"

/clone="F830034E13"

/tissue types="activated spleen"

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Best Local Similarity 87.1%; Pred. No. 2.2e-140;

Matches 602; Conservative 0; Mismatches 3; Indels 86; Gaps 2;

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DB 26 ATGGTGCTTTGCTGGCGCTGCGGCTATGGGCTGTGTGTCAGCGGTCCATCTA 85

QY 61 GGGCAGTGTTACGTGACGTGACAAACAGTACCTCCAGCAGTGGCCAGTCTGTGATTG 120

DB 86 GGGCAGTGTTACGTGACGTGACAAACAGTACCTCCAGCAGTGGCCAGTCTGTGATTG 145

QY 121 TGGCAGCCGAGGACCGACTGACAGCCACTGACAGCTCTTGAGAGACCAATGCCAC 180

DB 146 TGGCAGCCGAGGACCGACTGACAGCCACTGACAGCTCTTGAGAGACCAATGCCAC 205

QY 181 CCACTGTGACTCAGCGCAATTTCTCAGCCAGTGGAAACAGGGAGATTCGCTGTCCACGAC 240

DB 206 CCACTGTGACTCAGCGCAATTTCTCAGCCAGTGGAAACAGGGAGATTCGCTGTCCACGAC 265

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DB 362 AGCAAGGATTCGAGGAGGATGTCTCAGCACAGCCCTGTATCCCTGCTTTGGAGTTATG 421

QY 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTGTATCCCTGCCAGTCGGCTTCTCC 480

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# RESULT 4

LOCUS BY743050

DEFINITION BY743050 RIKEN full-length enriched, bone marrow macrophage Mus

musculus cDNA clone G530019M21 5', mRNA sequence.

ACCESSION BY743050

VERSION BY743050.1

KEYWORDS GI:27168930

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE

AUTHORS

REFERENCES

1 (bases 1 to 663)

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

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663 bp mRNA linear EST 17-DEC-2002

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

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## source

1. .663  
Location/Qualifiers  
/organism="Mus musculus"  
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Query Match 57.7%; Score 467; DB 13; Length 663;  
Best Local Similarity 86.9%; Pred. No. 7.6e-132;  
Matches 573; Conservative 0; Mismatches 0; Indels 86; Gaps 2;

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QY 61 GGCAGTGTCTTACGTGACAGCAACAGTACTCTCCAGATGCCAGTGGCTGTGATTG 120

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BY745486 RIKEN full-length enriched, bone marrow macrophage Mus  
musculus cDNA clone I830091M24 5', mRNA sequence.

Mus musculus (house mouse)

EST.

Source

ORGANISM

REFERENCE

AUTHORS

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12468851  
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## RESULT 6

BY751441

LOCUS

DEFINITION

BY751441

ACCESSION

BY751441.1

VERSION

KEYWORDS

SOURCE

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REFERENCE

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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

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Matches 497; Conservative 0; Mismatches 7; Indels 25; Gaps 2;  
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ACCESSION BF166137  
VERSION BF166137.1 GI:11046489  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 941)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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FEATURES  
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/note="Organ: lung; Vector: pCMV-SPORT6; Site.1: SalI; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

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Query Match 55.0%; Score 444.6; DB 10; Length 941;  
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427 GAGATGGCCACTGAGACCACTGATACCGTCTGTCTATCCCTGCCAGTCGGCTTCTTCCTCC 486
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ACCESSION CB547441
VERSION nr0g1-00106-f8 5', mRNA sequence.
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
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ACCESSION CB547441
VERSION nr0g1-00106-f8 5', mRNA sequence.
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00106 row: f column: 8.

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ACCESSION BY211683
VERSION BY211683.1 GI:26392288
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS

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Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
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Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
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Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
PUBMED
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
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Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

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prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

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## RESULT 14

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CDNA clone F83006D03 5', mRNA sequence.

## ACCESSION

## BY211594

## VERSION

## BY211594.1

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp  
URL: <http://genome.gsc.riken.go.jp/>  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ono, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.



QY	241	AGACACTGTGAACCCAGTGGTGGGCTGCCTGGGAAGGATCAAGGGCTTCGGGTTAAG	300
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Splice variants of cd40-receptor  
Patent: WO 0105967-A 6 25-JAN-2001:



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QY 601 CTATATCAAAAAGGTGGTCAAGAAACCAAGAGATATGAGATGTTACCCCTGCGGCTCG 660
Db 583 CTATATCAAAAAGGTGGTCAAGAAACCAAGAGATATGAGATGTTACCCCTGCGGCTCG 642
QY 661 AGGCAAGATCCCGAGGAGATGAAGATATCCCGGTCTAATACCGGTCTCCAGTGCA 720
Db 643 AGGCAAGATCCCGAGGAGATGAAGATATCCCGGTCTAATACCGGTCTCCAGTGCA 702
QY 721 GGAGACACTGCGCGGTGTGAGCTGTACACAGAGAGATGTTAAAGAGTTCGCATCTC 780
Db 703 GGAGACACTGCGCGGTGTGAGCTGTACACAGAGAGATGTTAAAGAGTTCGCATCTC 762
QY 781 AGTGAGAGCGCGCAGGTGACAGACAGCA 809
Db 763 AGTGAGAGCGCGCAGGTGACAGACAGCA 791

RESULT 3
AX077880
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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ORIGIN
Query Match
Best Local Similarity 91.7%; Score 742; DB 6; Length 776;
Matches 776; Conservative 0; Mismatches 0; Indels 24; Gaps 1;
QY 1 ATGGTGTCTTTTCCCTCGGCTGTGCGGCTATCGGCTGCTTTCACAGCGGTCCATCTA 60
Db 1 ATGGTGTCTTTTCCCTCGGCTGTGCGGCTATCGGCTGCTTTCACAGCGGTCCATCTA 60
QY 61 GGGCAGTGTGTACGTGACAGTACAAAAGTACCTCCAGATGGCGAGTGTGTGATTTG 120
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Db 277 AAGAGAGGCGACCGCAGAAATCAGACACTGTCTGTACCTGTAAAGGAAGACAACTGCAC 336
QY 361 AGCAAGATTCGAGAGGATGTCTCAGCACACGCGCTGTATCCCTGCTTTGGAGTTATG 420
Db 337 AGCAAGATTCGAGAGGATGTCTCAGCACACGCGCTGTATCCCTGCTTTGGAGTTATG 396
QY 421 GAGATGCGCACTGAGACCACTGATACCGTCTGTCTATCCCTGCGGCTTCTTCTCC 480
Db 397 GAGATGCGCACTGAGACCACTGATACCGTCTGTCTATCCCTGCGGCTTCTTCTCC 456
QY 481 AATCAGTCACTCACTTTTCGAAAAGTGTATCCCTGGAACAAGTTTAAAGTCCCGGATCG 540
Db 457 AATCAGTCACTCACTTTTCGAAAAGTGTATCCCTGGAACAAGTTTAAAGTCCCGGATCG 516
QY 541 AGCCCTGCTGTCATCTCTGTGATGGCATCCTCATCACATTTTCGGGGTGTCTTCT 600
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QY 601 CTATATCAAAAAGGTGTCTCAAGAAACCAAGAGATATGAGATGTTACCCCTGCGGCTCG 660
Db 577 CTATATCAAAAAGGTGTCTCAAGAAACCAAGAGATATGAGATGTTACCCCTGCGGCTCG 636
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Db 697 GGAGACACTGCGCGGTGTGAGCTGTACACAGAGAGATGTTAAAGAGTTCGCATCTC 756
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Db 757 AGTGAGAGCGGCGAGGTGA 776

RESULT 4
BD237352
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS
PN
PD
PF
PR
ROBERT IAN LECHLER, NICHOLA JANE ROGERS, ANTHONY DORLING PC
C12N15/09, A61K39/00, A61P37/06, C07K16/28, C12P21/08, C12N15/00 CC
Improvement in tolerance to xenografts
FH
FT
FEATURES
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Location/Qualifiers
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Query Match 83.9%; Score 679; DB 6; Length 870;		SOURCE Mus musculus (house mouse)	
Best Local Similarity 90.1%; Pred. No. 4.1e-203;		ORGANISM Mus musculus	
Matches 785; Conservative 0; Mismatches 0; Indels 86; Gaps 2;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		REFERENCE	
		Rogers, N.J., Dorling, A. and Lechler, R.I.	
		Immunosuppression	
		Patent: WO 0037102-A 11 29-JUN-2000;	
		ROGERS NICHOLA JANE (GB); DORLING ANTHONY (GB); ML LAB PLC (GB);	
		LECHLER ROBERT IAN (GB)	
		FEATURES	
		Location/Qualifiers	
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ORIGIN		Query Match 83.9%; Score 679; DB 6; Length 870;	
		Best Local Similarity 90.1%; Pred. No. 4.1e-203;	
		Matches 785; Conservative 0; Mismatches 0; Indels 86; Gaps 2;	
QY	1	ATGTTGCTTTTGGCTGGCTGTGGCGCTATGGGCTGTGTTGACAGCGGTCCATCTA	60
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QY	61	GGGCGAGTGTAGTGCAGTGAACAACAGTACTCCAGATGGCCAGTGTGTTGTTG	120
DB	61	GGGCGAGTGTAGTGCAGTGAACAACAGTACTCCAGATGGCCAGTGTGTTGTTG	120
QY	121	TGCCAGCCAGGAAGCCGACTGACAGCCACTGACAGCTCTTGAGAGAACCAATGCCAC	180
DB	121	TGCCAGCCAGGAAGCCGACTGACAGCCACTGACAGCTCTTGAGAGAACCAATGCCAC	180
QY	181	CCATGTGACTCAGCGCAATTCAGCCAGTGAACAGGAGATTCGCTGTACCAAGCAC	240
DB	181	CCATGTGACTCAGCGCAATTCAGCCAGTGAACAGGAGATTCGCTGTACCAAGCAC	240
QY	241	AGACACTGTGAACCCAGTGGCGCTGCTGGAGGAGTCAAGGGCTTCGGGTTAAG	300
DB	241	AGACACTGTGAACCCAGTGGCGCTGCTGGAGGAGTCAAGGGCTTCGGGTTAAG	300
QY	301	AAGAGGGGCAACCGAGCAATCAGACACTGTCTGTACCTGTAAAGAGAACCACTGCACC	360
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QY	361	AGCAAGGATTCGAGGCAATTCAGCCAGTGAACAGGAGATTCGCTGTACCAAGCAC	420
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QY	421	GAGATGGCCACTGAGACCACTGATACCGTGTGTATCCCTGCCAGTGGCTTCTTCTCC	480
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QY	521	-----GGTTTAAAGTCCCGGATG	538
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QY	637	CTCTATATCAAAAAGTGTCAAGAAACCAAGGATATGAGATGTACCCCTTCGGCT	696
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QY	659	CGACGGCAAGATCCCGAGGAGATGAAGATTTATCCCGTGTATACACCGCTGTCCAGTG	718
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QY	697	CGACGGCAAGATCCCGAGGAGATGAAGATTTATCCCGTGTATACACCGCTGTCCAGTG	756
DB	697	CGACGGCAAGATCCCGAGGAGATGAAGATTTATCCCGTGTATACACCGCTGTCCAGTG	756

RESULT 5  
AX027014  
LOCUS AX027014  
DEFINITION Sequence 11 from Patent WO0037102.  
ACCESSION AX027014  
VERSION AX027014.1 GI:10186044

AX027014 870 bp DNA linear PAT 16-SEP-2000  
Sequence 11 from Patent WO0037102.  
AX027014  
AX027014.1 GI:10186044

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QY 719 CAGGAGACACTGCACGGGTGTGAGCCTGTGCACACAGGAGGATGGTAAAGAGAGTGGCATC 778
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RESULT 6
AX708386
LOCUS AX708386 1579 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 17 from Patent WO02061135.
ACCESSION AX708386
VERSION AX708386.1 GI:29564273
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Lorenz, M.
TITLE Dna array sequence selection
JOURNAL Patent: WO 02061135-A 17 08-AUG-2002;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source Location/Qualifiers
1..1579
/organism="Mus musculus"
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ORIGIN
Query Match 83.9%; Score 679; DB 6; Length 1579;
Best Local Similarity 90.1%; Pred. No. 4.4e-203;
Matches 785; Conservative 0; Mismatches 0; Indels 86; Gaps 2;
QY 1 ATGGTGCTCTTGGCTCGGCTGTGGCGGTATGGGCTGCTTTCACAGCGGTCCATCTA 60
Db 9 ATGGTGCTCTTGGCTCGGCTGTGGCGGTATGGGCTGCTTTCACAGCGGTCCATCTA 68
QY 61 GGGCAGTGTGTACGTGCAGTGCACAAAGTACCTCCACAGTGGCGAGTGTGATTTG 120
Db 69 GGGCAGTGTGTACGTGCAGTGCACAAAGTACCTCCACAGTGGCGAGTGTGATTTG 128
QY 121 TGCCAGCCAGGAGCGGCTGTGACGCCACTGTGACAGCTCTTGAGAGACCCCAATGCCAC 180
Db 129 TGCCAGCCAGGAGCGGCTGTGACGCCACTGTGACAGCTCTTGAGAGACCCCAATGCCAC 188
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QY 241 AGACACTGTGAACCCAGTGGCTGGGCTGCCCTGGGAGGGATCAAGGGCTTCGGGTTAAG 300
Db 249 AGACACTGTGAACCCCA-----ATCAAGGGCTTCGGGTTAAG 284
QY 301 AAGAGGGGACCCGAGAAATTCAGACACTGTCTGTACCTGTGAAGGAAGGACCACTGCGACC 360
Db 285 AAGAGGGGACCCGAGAAATTCAGACACTGTCTGTACCTGTGAAGGAAGGACCACTGCGACC 344
QY 361 AGCAAGGATTCGAGGCATGTGTGACGACAGCGCTGTATCCCTGGCTTTGGAGTTATG 420
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521 -----GTTTAAAGTCCCGGATG 538
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RESULT 7
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LOCUS MUSCD40A 1579 bp mRNA linear ROD 23-SEP-1996
DEFINITION Mouse CD40 mRNA, complete cds.
ACCESSION M83312
VERSION M83312.1 GI:1553058
KEYWORDS CD40 antigen.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1579)
TITLE Differential increase of an alternatively polyadenylated mRNA
JOURNAL species of murine CD40 upon B lymphocyte activation
MEDLINE J. Immunol. 148 (2), 620-626 (1992)
PUBMED 92105763
REFERENCE 2 (bases 1 to 1579)
AUTHORS Grimaldi, J.C., Torres, R., Kozak, C.A., Chang, R., Clark, E.A.,
Howard, M. and Cockayne, D.A.
TITLE Genomic structure and chromosomal mapping of the murine CD40 gene
JOURNAL J. Immunol. 149 (12), 3921-3926 (1992)
MEDLINE 93094586
PUBMED 1281194
REFERENCE 3 (bases 1 to 1579)
AUTHORS Torres, R.M.
TITLE Direct Submission
JOURNAL Submitted (17-SEP-1996) Raul M. Torres, Basel Institute for
Immunology, Basel, CH-4005, Switzerland
COMMENT On Sep 23, 1996 this sequence version replaced gi:192519.
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 polyA\_site

ORIGIN

Query Match 83.9%; Score 679; DB 10; Length 1579;  
 Best Local Similarity 90.1%; Pred. No. 4.4e-203;  
 Matches 785; Conservative 0; Mismatches 0; Indels 86; Gaps 2;

QY 1 ATGCTGTCTTTCCTCGCTGTGGCGCTATGGGCTGCTGTGTGACAGGGTCCATCTA 60  
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 QY 61 GGGCAGTGTGTACGTGACAGTGAACAACAGTACTCTCCACGATGCCAGTGTCTGTGATTG 120  
 DB 69 GGGCAGTGTGTACGTGACAGTGAACAACAGTACTCTCCACGATGCCAGTGTCTGTGATTG 128  
 QY 121 TGCAGCAGGAGAGCCGACTGACAGCCACTGCACAGCTCTTGAGAGAGACCCATGCCAC 180  
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 DB 825 TCAGTGAGGAGCGGAGGTCAGACAGCA 855

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DEFINITION  
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 mRNA (CDNA clone MGC:36032 IMAGE:4018221), complete cds.

ACCESSION  
 BC029254

VERSION  
 BC029254.1

KEYWORDS  
 MGC.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

REFERENCE  
 1 (bases 1 to 1281)

AUTHORS  
 Strausberg, R.B., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences

JOURNAL  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE  
 22388257

PUBMED  
 12477932

REFERENCE  
 2 (bases 1 to 1281)

AUTHORS  
 Strausberg, R.

TITLE  
 Direct Submission

JOURNAL  
 Submitted (01-MAY-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue procurement: Gilbert Smith, Ph.D.  
 CDNA library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: the I.M.A.G.E. Consortium (ILLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Guaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 61 Row: h Column: 14  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 24850128.  
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 /tissue\_type="Mammary tumor metastasized to lung. Tumor

FEATURES  
 source

arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMV. "

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343. .459

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/db\_xref="CDD:smart00208"

ORIGIN

Query Match 82.3%; Score 666.2; DB 10; Length 1281;

Best Local Similarity 89.2%; Pred. No. 4.9e-199;

Matches 777; Conservative 0; Mismatches 8; Indels 86; Gaps 2;

QY 1 ATGGTGTCTTGGCTCGGCTGCGGCTATGGGCTGCTTGTACAGCGGTCCATCTA 60

DB 31 ATGGTGTCTTGGCTCGGCTGCGGCTATGGGCTGCTTGTACAGCGGTCCATCTA 90

QY 61 GGGCAGTGTGTACGTGAGTGACAAACAGTACTCCAGATGGCAGTGTGTGATTG 120

DB 91 GGGCAGTGTGTACGTGAGTGACAAACAGTACTCCAGATGGCAGTGTGTGATTG 150

QY 121 TGCACCCAGGAGCGGCTGACAGCCACTGCAGCTCTTGAGAAGACCAATGCCAC 180

DB 151 TGCACCCAGGAGCGGCTGACAGCCACTGCAGCTCTTGAGAAGACCAATGCCAC 210

QY 181 CCATGTGACTCAGGCGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCCACGAC 240

DB 211 CCATGTGACTCAGGCGAATTCTCAGCCAGTGGAAACAGGAGATTGCTGTCCACGAC 270

QY 241 AGACACTGTGAACCCAGTGGGCTGCTGGGAGGATCAAGGCTTCGGGTAAAG 300

DB 271 AGACACTGTGAACCCCA-----ATCAAGGGCTTCGGGTAAAG 306

QY 301 AAGGAGGCGACCCGAGAATCAGACACTGTCTGTACTGTAAAGAGGACCAACTGCACC 360

DB 307 AAGGAGGCGACCCGAGAATCAGACACTGTCTGTCTGTAAAGAGGACCAACTGTACC 366

QY 361 AGCAAGATTGGAGCATGTCTCAGACAGCCCTGTATCCCTGGCTTTGGAGTTATG 420

DB 367 AGCAAGATTGGAGCATGTCTCAGACAGCCCTGTATCCCTGGCTTTGGAGTTATG 426

QY 421 GAGATGGCCACTGAGACCACTGATACCGTGTCTATCCCTGCCAGTCCGCTTCTTCC 480

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QY 481 AATCAGTCATCACTTTTCGAAAAGTGTATCCCTGGACAA----- 520

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Db 607 CGAGCCCTGCTGTCATTCTCTGTCGATGGGATCTCTCATCACCATTTCGGGGTGTGTT 666

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Db 787 CAGGAGACCTGTCACGGGTGTCCAGCTGTCCACAGAGGATGCTAAAGAGAGTCCGATC 846

QY 779 TCAGTCAGGCGGCGAGGTGACAGACGCA 809

Db 847 TCAGTCAGGCGGCGAGGTGACAGACGCA 877

RESULT 9

MMU401389 926 bp mRNA linear ROD 01-JUN-2001

LOCUS Mus musculus mRNA for CD40 type IV isoform (CD40 gene).

DEFINITION

ACCESSION AJ401389

VERSION AJ401389.1 GI:13016733

KEYWORDS alternative splicing; CD40 gene; CD40 type IV isoform.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Tone, M., Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H.

Regulation of CD40 function by its isoforms generated through alternative splicing

Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)

2117110

PUBMED 11172023

REFERENCE 2 (bases 1 to 926)

Tone, M.

Direct Submission

Submitted (19-JUL-2000) Tone M., Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, UNITED KINGDOM

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 81.5%; Score 659; DB 10; Length 926;

Best Local Similarity 89.6%; Pred. No. 8.9e-197;

Matches 780; Conservative 0; Mismatches 0; Indels 91; Gaps 3;



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RESULT 10  
NMU401390  
LOCUS NMU401390 844 bp mRNA linear ROD 01-JUN-2001  
DEFINITION Mus musculus mRNA for CD40 type V isoform (CD40 gene).  
ACCESSION AJ401390  
VERSION AJ401390.1 GI:13016735  
KEYWORDS alternative splicing; CD40 gene; CD40 type V isoform.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1  
Tone, M., Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H.  
Regulation of CD40 function by its isoforms generated through  
alternative splicing  
Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)  
21117110  
PUBMED 11172023  
2 (bases 1 to 844)  
Tone, M.  
Direct Submission  
Submitted (19-JUN-2000) Tone M., Sir William Dunn School of  
Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE,  
UNITED KINGDOM  
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RESULT 11
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LOCUS          Mus musculus mRNA for CD40 type III isoform (CD40 gene).
DEFINITION     AJ401388
ACCESSION      AJ401388.1 GI:13016731
VERSION        alternative splicing; CD40 gene; CD40 type III isoform.
KEYWORDS       Mus musculus (house mouse)
SOURCE         Mus musculus
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1
AUTHORS        Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H.
TITLE          Regulation of CD40 function by its isoforms generated through
               alternative splicing
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)
MEDLINE        21117110
PUBMED         11172023
REFERENCE      2 (bases 1 to 1032)
AUTHORS        Tone, M.
TITLE          Direct Submission
JOURNAL        Submitted (19-JUL-2000) Tone M., Sir William Dunn School of
               Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE,
               UNITED KINGDOM
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## FEATURES

source

## gene

## CDS

## ORIGIN

Query Match 70.2%; Score 568; DB 10; Length 1032;  
 Best Local Similarity 80.8%; Pred. No. 5.8e-168;

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Qy 61 GGGCAGTGTGTTACGTGTCAGTGAACACAGTACTCTCCAGATGCGCCAGTCTGTGATTG 120
Db 67 GGGCAGTGTGTTACGTGTCAGTGAACACAGTACTCTCCAGATGCGCCAGTCTGTGATTG 126
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Db 127 TGGCAGCAGGAGCGGCTGACAGCCACTGACAGCTCTTGGAGAGACCCCAATGCCAC 186
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Qy 361 AGCAAGGATTGCGAGGATGTGTCAGCAACGCGCTGTATCCCTGCTTGGAGTTATG 420
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Qy 421 GAGATGCCACTGAGACCACTGATACCGTCTGTACCTGCCAGTCCGCTTCTCTCC 480
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Qy 481 AATCAGTCATCACTTTTTCGAAAAGTGTATCCCTGGACAA----- 520
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Qy 738 GTCAGCCTGTCAACAGAGGAGTGGTAAAGAGAGTTCGCATCTCTCAGTGCAGGAGCGGAGG 797
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RESULT 12  
 AX077881

LOCUS AX077881 788 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 5 from Patent WO0105967.  
 ACCESSION AX077881  
 VERSION AX077881.1 GI:13157728  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Savitzky, K., Khosravi, R. and Elazar, M.  
 TITLE Spice variants of cd40-receptor  
 JOURNAL Patent: WO 0105967-A 5 25-JAN-2001;  
 Compugen Ltd. (IL)  
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 QY 1 ATGTGTCTTTGCTCGGCTGTGGCGCTATGGGCTGTGTTGACAGCGGTCCATCTA 60  
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 Db 241 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 276  
 QY 301 AAGAGGGCCACCGAGATCAGACACTGTGTACCTGTAGAGAGAGAGAGAGAGAGAG 360  
 Db 277 AAGAGGGCCACCGAGATCAGACACTGTGTACCTGTAGAGAGAGAGAGAGAGAGAG 336  
 QY 361 AGCAAGGATTGCGAGGATGTGTGACACACGCGCTGTATCCCTGGCTTTGAGTTATG 420  
 Db 337 AGCAAGGATTGCGAGGATGTGTGACACACGCGCTGTATCCCTGGCTTTGAGTTATG 396  
 QY 421 GAGATGCCACTGAGACCACTGATACCGTGTGTATCCCTGCCAGTGGCTTCTTCTCC 480  
 Db 397 GAGATGCCACTGAGACCACTGATACCGTGTGTATCCCTGCCAGTGGCTTCTTCTCC 456  
 QY 481 AATCAGTCACTCACTTTTCGAAAGTGTATCCCTGGCAAGGTTTAAAGTCCCGGATGCG 540  
 Db 457 AATCAGTCACTCACTTTTCGAAAGTGTATCCCTGGCAAGGTTTAAAGTCCCGGATGCG 516  
 QY 541 AGCCTCTGCTCATTCCTGTGTGATGGGATCCTCATCACCATTTCGGGGTGTTCCT 600  
 Db 517 AGCCTCTGCTCATTCCTGTGTGATGGGATCCTCATCACCATTTCGGGGTGTTCCT 576  
 QY 601 CTATATCAAAAAG 613  
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RESULT 13  
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DEFINITION Sequence 3 from Patent WO0105967.  
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 VERSION AX077879.1 GI:13157726  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Savitzky, K., Khosravi, R. and Elazar, M.  
 TITLE Spice variants of cd40-receptor  
 JOURNAL Patent: WO 0105967-A 3 25-JAN-2001;  
 Compugen Ltd. (IL)  
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 QY 1 ATGTGTCTTTGCTCGGCTGTGGCGCTATGGGCTGTGTTGACAGCGGTCCATCTA 60  
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 Db 273 AGACACTGTGAACCCA-----ATCAAGGGCTTCGGGTTAAG 308  
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 LOCUS  
 DEFINITION Rattus norvegicus CD40 protein mRNA, partial cds.

ACCESSION AF241231  
VERSION AF241231.2 GI:13400107  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 225 to 547)  
REFERENCE Krzesz.R., Wagner.A.H., Cattaruzza,M. and Hecker,M.  
AUTHORS Cytokine-inducible CD40 gene expression in vascular smooth muscle  
TITLE cells is mediated by nuclear factor kappaB and signal transducer  
and activation of transcription-1  
JOURNAL FEBS Lett. 453 (1-2), 191-196 (1999)  
MEDLINE 99330195  
PUBMED 10403401  
REFERENCE 2 (bases 225 to 547)  
AUTHORS Krzesz.R. and Hecker.M.  
TITLE Direct Submission  
JOURNAL Submitted (02-MAR-2000) Dept. of Cardiovascular Physiology, Univ.  
of Goettingen, Humboldtallee 23, Goettingen 37073, Germany  
REFERENCE 3 (bases 1 to 547)  
AUTHORS Gao,D. and Hecker,M.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-2001) Dept. of Cardiovascular Physiology, Univ.  
of Goettingen, Humboldtallee 23, Goettingen 37073, Germany  
REMARK Sequence update by submitter  
COMMENT On Mar 21, 2001 this sequence version replaced gi:7248905.  
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Best Local Similarity 84.7%; Pred. No. 1.3e-108;  
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DEFINITION Sequence 2460 from Patent WO03039443.  
ACCESSION AX780303  
VERSION AX780303.1 GI:32697297  
KEYWORDS Homo sapiens (human)  
SOURCE ORGANISM  
Homo sapiens  
Homo sapiens  
REFERENCE 1  
AUTHORS Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,  
Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.  
TITLE Novel genetic markers for leukemias  
JOURNAL Patent: WO 03039443-A 2460 15-MAY-2003;  
Deutsches Krebsforschungszentrum (DE);  
Ludwig-Maximilian-Universitaet Muenchen (DE);  
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)  
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Best Local Similarity 67.5%; Pred. No. 2.1e-99;  
Matches 537; Conservative 0; Mismatches 232; Indels 27; Gaps 2;  
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DB 149 TGCACGCCAGGAAGCCGACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 208  
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QY 301 AAGAGGGGACCGCAGAACTCAGACTGTGTGTAAGAGGAGACAACTGCGACC 360  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 21, 2004, 10:03:39 ; Search time 16 Seconds  
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Title: US-10-031-607-7

Perfect score: 913  
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Scoring table: BLOSUM62

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Listing first 45 summaries

Database : PIR 78:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	785	86.0	277	2 A60771	B-cell activation
2	483	52.9	305	2 A46476	B cell-associated
3	212.5	23.3	461	1 A33356	tumor necrosis fac
4	200	21.9	435	2 I54182	tumor necrosis fac
5	188.5	20.6	324	2 JC2395	Fas antigen precu
6	180	19.7	327	2 A46484	apoptosis-mediatur
7	174.5	19.1	459	2 I48854	gene murine tumour
8	173	18.9	474	2 B38634	tumor necrosis fac
9	170	18.6	349	2 D72175	G2R protein - vari
10	170	18.6	349	2 D38858	gene G2R protein -
11	167.5	18.3	260	1 A4517	CD27 antigen precu
12	167.5	18.3	348	2 T28623	hypothetical prote
13	165	18.1	335	2 A40036	apoptosis-mediatur
14	153	16.8	314	2 I37383	FAS soluble protei
15	151	16.5	250	1 A49053	CD27 antigen precu
16	145	15.9	271	2 S12783	OX40 antigen precu
17	142	15.6	272	2 I48700	gene OX40 protein
18	135.5	14.8	277	2 I37552	OX40 homolog - hum
19	130	14.2	416	1 JN0006	nerve growth facto
20	129.5	14.2	461	1 GQRT11	tumor necrosis fac
21	129	14.1	326	1 GOVZML	T2 protein - myxom
22	128.5	14.1	454	1 GQXST1	tumor necrosis fac
23	125.5	13.7	455	1 GQXST1	tumor necrosis fac
24	121	13.3	651	2 JCHUT1	death receptor-6 -
25	116	12.7	325	2 B43692	T2 protein - rabbi
26	115.5	12.7	427	1 GQHUN	nerve growth facto
27	111	12.2	1069	2 T42681	hypothetical prote
28	109.5	12.0	461	2 JC4302	tumor necrosis fac
29	109.5	12.0	1274	2 T42017	cysteine rich prot

nerve growth facto  
CDw40 antigen Hu54  
neurogenic protein  
gene Delta protein  
neurogenic repetit  
laminin beta-1 cha  
od2 protein - frul  
tenascin-like prot  
gene PACE4 protein  
serine proteinase  
mucin, submaxillar  
protein C34G6-2 [i  
Ncl-homolog protei  
PACE4A - mouse (fr  
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## ALIGNMENTS

### RESULT 1

A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C:Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.//  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:93356608; PMID:2475341  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:g29850; PID:CAA43045.1; PID:g29851  
R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:89093941; PMID:2463309  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics:  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CYT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 86.0%; Score 785; DB 2; Length 277;  
Best Local Similarity 95.1%; Pred. No. 5.8e-57;  
Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MVRPLQCVLWGCLLTAVHPPTACREKQVLYNSQCCSLCQPGQKLVSDCTETETECFL 60  
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QY 61 PCGSEFLDWNRTTHCHQHKYCDPNLGLRVQOQGTSETDTICTCEGWHCTSEACSECV 120  
DB 61 PCGSEFLDWNRTTHCHQHKYCDPNLGLRVQOQGTSETDTICTCEGWHCTSEACSECV 120  
QY 121 LHRSCSPGFQKQIAVRPKTWLC 143  
DB 121 LHRSCSPGFQKQIAVRPKTWLC 143

## RESULT 2

A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
C:Accession: A46476; A46515  
R:Torres, R.M.; Clark, E.A.  
J. Immunol. 146, 620-626, 1992  
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine A:Reference number: A46476; MUID:92105763; PMID:1370315  
A:Accession: A46476  
A:Molecule type: mRNA  
A:Status: Preliminary  
A:Residues: 1-305 <TOR>  
A:Cross-references: GB:M83312; NID:G1553058  
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)  
A:Note: this translation is not annotated in GenBank entry M55994, release 113.0.  
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992  
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
A:Reference number: A46515; MUID:93094586; PMID:1261194  
A:Accession: A46515  
A:Status: Preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-287, 'LV' <GRI>  
A:Cross-references: GB:M83312; NID:G1553058; PIDN:AA08705.1; PID:G1553059; GB:M94126; N  
A:Experimental source: BALB/c, liver  
A:Note: sequence extracted from NCBI backbone (NCBI:120357)  
C:Comment: For an alternative splice form, see PIR:A46515.  
C:Comment: For an alternative splice form, see PIR:A46476.  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: alternative splicing; transmembrane protein  
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 52.98; Score 483; DB 2; Length 305;  
Best Local Similarity 54.98; Pred. No. 2.4e-32;  
Matches 79; Conservative 21; Mismatches 44; Indels 0; Gaps 0;

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Db 61 PCDSGEFSQAWNRIQRCHQRCPEPQGLRVKKGTAESDTVCTCKEGQCTSKDCEACA 120

Qy 121 LHRSCSPGFGVKQIAVRPKTWLQN 144  
Db 121 QHTPCIFGFGVWENATTTTIVCH 144

## RESULT 3

A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 27-Oct-2003  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
Science 248, 1019-1023, 1990  
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A:Reference number: A35356; MUID:90260639; PMID:2160731  
A:Accession: A35356  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:G189185; PIDN:AAA59929.1; PID:G189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A:Reference number: A36475; MUID:91045991; PMID:2172983  
A:Accession: A36475

A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195, 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Cytokine 2, 231-237, 1990  
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:1966549  
A:Accession: A48416  
A:Status: Preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:G235648; PIDN:AA019824.1; PID:G235649  
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)  
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat A:Reference number: A36007; MUID:90349572; PMID:2166946  
A:Accession: A36007  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>  
A:Cross-references: GB:M55957; NID:G339751; PIDN:AA063262.1; PID:G339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990  
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec A:Reference number: A23666; MUID:91056048; PMID:2173696  
A:Accession: A23666  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 23-40; 65-89; 136-141; 300-306 <LOE>  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence i A:Reference number: A35010; MUID:90110215; PMID:2153136  
A:Accession: B35010  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 27-31 <ENG>  
R:Kuhnert, P.; Kemper, O.; Wallach, D.  
Gene 150, 381-386, 1994  
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of A:Reference number: I38094; MUID:95121934; PMID:7821811  
A:Accession: I38094  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-37 <RES>  
A:Cross-references: EMBL:X80021; NID:G666044; PIDN:CAA56324.1; PID:G825701  
C:Genetics:  
A:Gene: GDB:TNFR2  
A:Cross-references: GDB:125914; OMIM:191191  
A:Map position: 1p36.2-1p36.2  
A:Introns: 26/3  
A:Note: The list of introns is incomplete  
C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>  
F:40-76/Domain: NGF receptor repeat homology <NG1>  
F:78-119/Domain: NGF receptor repeat homology <NG2>  
F:120-162/Domain: NGF receptor repeat homology <NG3>  
F:164-201/Domain: NGF receptor repeat homology <NG4>  
F:262-279/Domain: transmembrane #status predicted <TMN>  
F:280-461/Domain: intracellular #status predicted <INT>  
F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.3%; Score 212.5; DB 1; Length 461;  
Best Local Similarity 34.5%; Pred. No. 3.6e-10;  
Matches 51; Conservative 12; Mismatches 58; Indels 27; Gaps 6;

Qy 4 LPQCVLWGLLTAVHPPEPTACRQKYLINS-CCSLCPQKQLVSDCTEFTTECLP 61  
Db 23 LPAQVA-----FTPAPEFGSTRLREIYDQIAQMCSCKSPGHAKVFTKTSITVCD 77

QY 62 CGESEFLDWNRETHCHQHKYCDNLGLRVQ-----QKGTSETDTTCTCEEGWHCT--- 112  
 Db 78 CEDSTYTQLMNVPEC-----LSCGSRCSDDQVETQACTREQNRICTRCPGWCALSK 130  
 QY 113 SEACESCVLHRS CSPGFGVKQIAPRPT 140  
 Db 131 QEGRLCAPLRKCRPGFGV-----ARPGT 154

## RESULT 4

154182  
 tumor necrosis factor receptor 2-related protein - human  
 C:Species: Homo sapiens (man)  
 C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
 C:Accession: I54182  
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
 Genomics 16, 214-218, 1993  
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen  
 A:Reference number: I54182; MUID:93252381; PMID:8486360  
 A:Accession: I54182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <RES>  
 A:Cross-references: GB:L04270; NID:g3339761; PIDN:AAA36757.1; PID:g3339762  
 C:Genetics: LITBR  
 A:Gene: GDB:LTBR  
 A:Cross-references: GDB:1230195; OMIM:600979  
 A:Map position: 12p13.3-12p13.1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 21.9%; Score 200; DB 2; Length 435;  
 Best Local Similarity 36.5%; Pred. No. 3.6e-09;  
 Matches 50; Conservative 15; Mismatches 58; Indels 14; Gaps 6;  
 QY 5 PLQCVLWGLTAVHPE--PPTA-----CR--EKQYLINSQ--CCSLQCPQKLVSDCTE 53  
 Db 16 PLVLGLFG-LLAASQPAVPPYASENQTCRQKEKYEPQHRICGSRCPGPGTVYSAKSR 74  
 QY 54 FTETSLCGSESEFLDWNRETHCHQHKYCDNLGLRVQKGTSETDTTCTCEEGWHCTS 113  
 Db 75 INDTVCATCAENSNEHWNLYTICQLCRPCDPVWGLBETAPCTSKRTQCRCPQGMCAA 134  
 QY 114 EA--CESCVLHRS CSPG 128  
 Db 135 WALECTHCELLSDCCPG 151

## RESULT 5

JC2395  
 Fas antigen precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Jul-2003  
 C:Accession: JC2395; PC2246  
 R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
 Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
 A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat live  
 A:Reference number: JC2395; MUID:94128114; PMID:7507668  
 A:Accession: JC2395  
 A:Molecule type: mRNA  
 A:Residues: 1-324 <KIM>  
 A:Cross-references: DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005650; PID:g468487  
 A:Experimental source: thymus  
 A:Accession: PC2246  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'RPT', <K12>  
 A:Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489  
 A:Experimental source: liver  
 C:Genetics:  
 A:Introns: 62/1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-324/Product: Fas antigen #status predicted <MAT>  
 F:44-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NG4>  
 F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 20.6%; Score 188.5; DB 2; Length 324;  
 Best Local Similarity 30.6%; Pred. No. 2.4e-08;  
 Matches 44; Conservative 20; Mismatches 69; Indels 11; Gaps 5;  
 QY 21 EPPTACREKQYLINSQCCLCPQKLVSDC-TEFTETELCPGE-SEFLDTWNRETHCH 78  
 Db 39 ETDNNCSEGLYQVGFPCQCPQGERKVKDCTTGGAPCTCHPCTEGEYVTRDKHYSKCR 98  
 QY 79 OHKQYCDPNLGLRVQKGTSETDTTCTCEEGWHCTSACESCVLHRS CSPGFGVKQI---A 135  
 Db 99 RCFAFCDEHGLEVETNCTRTQNTKCRKENFYCNASLCHDCHYCTSC-----GLEIDLEPC 154  
 QY 136 VRPKTWLCNRQAQT--RLMLSVVP 157  
 Db 155 TRTSNTKCKQSSNYKLLWLLIIP 178

## RESULT 6

A46484  
 apoptosis-mediating membrane-associated polypeptide Fas - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Jul-2003  
 C:Accession: A46484; R:7254  
 R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J.; Immunol. 148, 1274-1279, 1992  
 A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas anti  
 A:Reference number: A46484; MUID:92148151; PMID:1371136  
 A:Accession: A46484  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-327 <MAT>  
 A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
 A:Experimental source: BAM3 macrophage cell line  
 A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
 R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
 A:Title: Aberrant transcription caused by the insertion of an early transposable element  
 A:Reference number: A47254; MUID:93189576; PMID:7680478  
 A:Accession: A47254  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-96 <ADA>  
 A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506  
 A:Experimental source: MRL lpr/lpr  
 A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863,  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:44-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 19.7%; Score 180; DB 2; Length 327;  
 Best Local Similarity 33.6%; Pred. No. 1.2e-07;  
 Matches 49; Conservative 15; Mismatches 68; Indels 14; Gaps 6;  
 QY 18 VHPPTACREKQYLINSQCCLCPQKLVSDCTETET-ECILPCGE-SEFLDTWNRET 75  
 Db 37 VH-ETDKNCSEGLYQGFPCQCPQGERKVKDCTTGGAPCTCHPCTEGEYVTRDKHYSKCR 95  
 QY 76 HCHQHKYCDPNLGLRVQKGTSETDTTCTCEEGWHCTSACESCVLHRS CSPGFGVKQIA 135  
 Db 96 KCRRTCLCDEHGLEVETNCTRTQNTKCRKENFYCNASLCHDCHYCTSC-----T 149  
 QY 136 VRPKTWL-----CNRQA--OTRMLSVV 156  
 Db 150 LEPCTATSNTRCKQSPNRNLWLLTI 175

## RESULT 7



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Query Match      18.9%; Score 173; DB 2; Length 474;
Best Local Similarity 28.6%; Pred. No. 6e-07;
Matches 42; Conservative 21; Mismatches 64; Indels 20; Gaps 6;

QY      2 VRLPQCVLWG-----CLTAVHPPEPTACREKQYLYN--SQCCSLCOPGQKLVSD 50
Db      8 VALVFELQWATGHTVPAQVVLTPYKPEFGYECQISQEIYDRKQCMCAKPPQYVQHF 67

QY      51 CTEFTETELPCGSEBFLDTWNRETHQHXYCDPNLGLRVQQKG-TSETDTICTCEEG 108
Db      68 CNKTSDTVCADCEASMYQVAVNQFRTCLIS--CSSCTTDQVEIRACTKQQRVYCAEAG 124

QY      109 WHCT-----SEACSCVLHRSCTPGFGV 131
Db      125 RYCALKTHSGSCRCQCMRLSKCGPGFGV 151

RESULT 9
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 15-Sep-2003
C:Accession: D72175
R:R.Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Loparev, S.G.;
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GS:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: G2R
A:C:Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match      18.6%; Score 170; DB 2; Length 349;
Best Local Similarity 29.0%; Pred. No. 8.3e-07;
Matches 38; Conservative 21; Mismatches 64; Indels 8; Gaps 4;

QY      6 LQCVLWGLLTAVHPEPTACREKQYLYNQCCLCOPGQKLVSDCTFTETELPCGES 65
Db      12 LSCIINGRDAAPTPNGKCKOTEYKRNHLCCLSCPPGTYASRLCDSKINTQCTPCGSG 71

QY      66 EFLDTWNRETHCQ-HKYCDPNLGRVQQKGTSET-DTICTCEGWHCT---SEACSCV 120
Db      72 TFTSENHLPALCSNGRCNSN---QVETRSCNTHNRICECSPGYICLLKSGSGCACV 128

QY      121 LHRSCSPGFGV 131
Db      129 SQTCKGIGYGV 139

RESULT 10
D36858
Gene G4R protein - variola virus
A:Name: G4R protein
A:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087
A:Experimental source: strain India-1967, sep. major, isolate Ind3
R:R.Kolykhalov, A.A.; Blinov, V.M.; Gutorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, A.;
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P C

```



A;Reference number: S46868

A;Accession: S46888

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-349 <COL>

A;Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449

A;Experimental source: strain India-1967, isolate Ind3

R;Shchelkunov, S.N.; Blinov, V.M.; Sandakchiev, L.S.

FBS Lett. 319, 80-83, 1993

A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A;Reference number: S32385; MUID:93202281; PMID:8384129

A;Accession: S32385

A;Molecule type: DNA

A;Residues: 31-168 <SHC>

A;Cross-references: EMBL:X69198

A;Experimental source: strain India-1967, ssp. major

C;Genetics:

A;Gene: GAR

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F;32-66/Domain: NGF receptor repeat homology <NGF>

F;68-109/Domain: NGF receptor repeat homology <NG2>

F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match

Best Local Similarity 18.6%; Score 170; DB 2; Length 349;

Matches 38; Conservative 21; Mismatches 64; Indels 8; Gaps 4;

QY 6 LQVLWGCLLTAVHPEPTACREKQYVLSQ-CCSLCOPGKLVSDCTEFTETECCLPCGES 65

Db 12 LSCIINGRDAAPYTPNGKCKDTEYKRNLCCLSCPPGTAYASRLCDSKNTQCTPCSG 71

QY 66 EFLDTWNRETHCHQ-HKYCDPNLGLRVQOKGSET-DTICTCEEGWHCT---SEACEBSCV 120

Db 72 TFTSRNHLPACLSCNGRCNSN---QVETRSCNTHNRICEGSPGYVCLLKSGSGCKACV 128

QY 121 LHRSCSPGFGV 131

Db 129 SQTCKGIGYGV 139

RESULT 11

A46517

CD27 antigen precursor - human

N;Alternate names: CD27L receptor; T cell activation antigen CD27

C;Species: Homo sapiens (man)

C;Date: 18-Jun-1993 #sequence\_revision 22-Apr-1995 #text\_change 22-Jun-1999

C;Accession: A46517; A46454

R;Loenen, W.A.; Gravesstein, L.A.; Beumer, S.; Melief, C.J.; Hagemeijer, A.; Borst, J.

J. Immunol. 149, 3937-3943, 1992

A;Title: Genomic organization and chromosomal localization of the human CD27 gene.

A;Reference number: A46517; MUID:93094588; PMID:1334106

A;Accession: A46517

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-260 <LOE>

A;Note: sequence extracted from NCBI backbone (NCBIP:120386)

A;Note: authors propose an alternative repeat pattern

R;Camerini, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.

J. Immunol. 147, 3165-3169, 1991

A;Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumor

A;Reference number: A46454; MUID:92013149; PMID:1655907

A;Accession: A46454

A;Molecule type: mRNA

A;Residues: 1-58, A, 60-260 <CM>

A;Cross-references: GB:M63928; NID:G180084; PIDN:AAA58411.1; PID:G180085

A;Note: sequence extracted from NCBI backbone (NCBIN:50285, NCBIP:50289)

C;Comment: A soluble CD27 found in serum and urine is formed by proteolysis.

C;Genetics:

A;Gene: GDB:CD27

A;Cross-references: GDB:132582; OMIM:186711

A;Map position: 12p13-12p13

A;Introns: 46/1; 90/1; 150/1; 180/1; 220/1

C;Superfamily: CD27 antigen; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; homodimer; phosphoprotein; receptor; surface anti  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-260/Product: CD27 antigen #status predicted <MAT>  
F;21-191/Domain: extracellular #status predicted <EXT>  
F;27-63/Domain: NGF receptor repeat homology <NG1>  
F;65-105/Domain: NGF receptor repeat homology <NG2>  
F;121-188/Region: proline/serine/threonine-rich  
F;192-211/Domain: transmembrane #status predicted <TMN>  
F;212-260/Domain: intracellular #status predicted <INT>  
F;95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.3%; Score 167.5; DB 1; Length 260;

Best Local Similarity 34.5%; Pred. No. 1.1e-06;

Matches 40; Conservative 15; Mismatches 52; Indels 9; Gaps 7;

QY 8 CVLWGCLLTAVHPEPTACREKQYVLSQ-CCSLCOPGKLVSDCTEFTET-ECLPC--G 63

Db 10 CVL-GTLVGLSATPAPKSCPERHYWAQKLCQCCCEFTLVKDCDQHRKTAQCDPIPG 68

QY 64 ESEFLDTWNRETHCHQHYCDPNLGLRVQOKGSETDTICTCEEGWHCTSEACEBSCV 119

Db 69 VS-FSPDHTRPHCESCRHC--NSGLLV-RNCTITANAECACRNGMQCRDKCTEC 120

RESULT 12

T28623

hypothetical protein G2R - variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 15-Sep-2003

C;Accession: T28623

R;Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin,

Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus

A;Reference number: 220488; MUID:94088747; PMID:8264798

A;Accession: T28623

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-348 <MAS>

A;Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60933.1; PID:G439102

A;Experimental source: strain Bangladesh 1975

C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 18.3%; Score 167.5; DB 2; Length 348;

Best Local Similarity 29.8%; Pred. No. 1.3e-06;

Matches 39; Conservative 21; Mismatches 62; Indels 9; Gaps 5;

QY 6 LQVLWGCLLTAVHPEPTACREKQYVLSQ-CCSLCOPGKLVSDCTEFTETECCLPCGES 65

Db 12 LSCIINGRDAAPYTPNGKCKDTEYKRNLCCLSCPPGTAYASRLCDSKNTQCTPCSG 70

QY 66 EFLDTWNRETHCHQ-HKYCDPNLGLRVQOKGSET-DTICTCEEGWHCT---SEACEBSCV 120

Db 71 TFTSRNHLPACLSCNGRCNSN---QVETRSCNTHNRICEGSPGYVCLLKSGSGCKACV 127

RESULT 13

A40036

apoptosis-mediating surface antigen Fas precursor - human

N;Alternate names: surface antigen APO-1

C;Species: Homo sapiens (man)

C;Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 07-Jul-2003

C;Accession: A40036; S24543; A38142

R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase,

Cell 66, 233-243, 1991

A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can medi

A;Reference number: A40036; MUID:91309137; PMID:1713127

A;Accession: A40036

A;Status: preliminary

A;Molecule type: mRNA

A:Residues: 1-335 <ITO>  
A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410  
R:Krammer, P.H.  
Submitted to the EMBL Data Library, February 1992  
A:Reference number: S24543  
A:Accession: S24543  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-335 <KRA>  
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742  
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich  
J. Biol. Chem. 267, 10709-10715, 1992  
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member  
A:Reference number: A38142; MUID:92268122; PMID:1375228  
A:Accession: A38142  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-134, 'Q', 136-335 <OE>  
A:Experimental source: SKW6.4 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)  
A:Note: in NCBI backbone the source is designated as mouse  
C:Genetics:  
A:Gene: GDB:APT1  
A:Cross-references: GDB:132671; OMIM:134637  
A:Map position: 10q24.1-10q24.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: apoptosis; surface antigen; transmembrane protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:185-128/Domain: NGF receptor repeat homology <NG4>  
F:174-190/Domain: transmembrane #status predicted <TMN>  
Query Match 18.1%; Score 165; DB 2; Length 335;  
Best Local Similarity 29.2%; Pred. No. 2e-06; Indels 22; Gaps 5;  
Matches 40; Conservative 18; Mismatches 57  
QY 37 CCSLCQPGKLVSDCT-EFTETCLPCGE-SFELDTWNRETHCHQHKYCDPNLGLRVQOK 94  
DB 59 CHKPCPPGERKARDCTVNGDEPDVCPQEGKEYTDKAHFSSKRCRLCDEGHGLEVEIN 118  
QY 95 GTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIAVRPKT-----WL 142  
DB 119 CTRTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGI-1KECTLTNT-KCKEVEK 177  
QY 143 CNROAQRLMLSVVPI 159  
DB 178 C-----LALLPIPLI 187  
RESULT 14  
137383  
FAS soluble protein - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 07-Jul-2003  
C:Accession: I37383  
R:Cascino, I.; Ficuci, G.; Papoff, G.; Ruberti, G.  
J. Immunol. 154, 2706-2713, 1995  
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are  
A:Reference number: I37383; MUID:95181785; PMID:7533181  
A:Accession: I37383  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-314 <RES>  
A:Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
Query Match 16.8%; Score 153; DB 2; Length 314;  
Best Local Similarity 29.3%; Pred. No. 1.8e-05;  
Matches 34; Conservative 19; Mismatches 59; Indels 4; Gaps 4;  
QY 37 CCSLCQPGKLVSDCT-EFTETCLPCGE-SFELDTWNRETHCHQHKYCDPNLGLRVQOK 94  
DB 59 CHKPCPPGERKARDCTVNGDEPDVCPQEGKEYTDKAHFSSKRCRLCDEGHGLEVEIN 118

QY 95 GTSETDTICTCEGWHCTSEACSVLHRSCTSPGFGVKQIAVRPKTLCNRQAQTR 150  
DB 119 CTRTQNTKCRCKPNFNCSTVCEHCDPCTKCEHGI-1KECTLTNT-KCKEVEK 172  
RESULT 15  
A49053  
CD27 antigen precursor - mouse  
N:Alternate names: CD27L receptor; T cell activation antigen CD27  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Dec-1993 #sequence\_revision 22-Apr-1995 #text\_change 11-Sep-1998  
C:Accession: A49053  
R:Graveststein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Osendorp, I.  
Eur. J. Immunol. 23, 943-950, 1993  
A:Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte  
A:Reference number: A49053; MUID:93209296; PMID:8384562  
A:Accession: A49053  
A:Molecule type: mRNA  
A:Residues: 1-250 <GRA>  
A:Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; trar  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-250/Product: CD27 antigen #status predicted <MAT>  
F:21-182/Domain: extracellular #status predicted <EXT>  
F:27-63/Domain: NGF receptor repeat homology <NGL>  
F:65-105/Domain: NGF receptor repeat homology <NG2>  
F:121-179/Region: proline/serine/threonine-rich  
F:183-202/Domain: transmembrane #status predicted <TMN>  
F:203-250/Domain: intracellular #status predicted <INT>  
F:95,162/Binding site: carbohydrate (asn) #status predicted  
Query Match 16.5%; Score 151; DB 1; Length 250;  
Best Local Similarity 28.2%; Pred. No. 2.2e-05;  
Matches 33; Conservative 18; Mismatches 54; Indels 12; Gaps 6;  
QY 11 WGLLTAV-----HPRPTACREKQVLI-NSOCCSLCQPGKLVSDC-TEFTETCLPC-- 62  
DB 8 WLCMLGLTVGLSALFAPNSCPDKHYWTGGGLCCRMCEGTFVVKDCBQDRAAQQDCIP 67  
QY 63 GESEFLDTWNRETHCHQHKYCDPNLGLRVQOKGSETDTICTCEGWHCTSEACESC 119  
DB 68 GTS-PSPDYHTRPHCESCRHNSGLIR---NCTVTANAEGSCSKNMQCRDQECTEC 120  
Search completed: July 21, 2004, 10:07:17  
Job time : 17 secs